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<b>(51) International Patent Classification <sup>7</sup> :</b> <b>C12N 15/12, A61K 38/17, C07K 14/47, 16/18, A61K 35/14, C12Q 1/68</b>	<b>A2</b>	<b>(11) International Publication Number:</b> <b>WO 00/60077</b> <b>(43) International Publication Date:</b> 12 October 2000 (12.10.00)												
<b>(21) International Application Number:</b> PCT/US00/08560 <b>(22) International Filing Date:</b> 30 March 2000 (30.03.00)  <b>(30) Priority Data:</b> <table border="0"><tr><td>09/285,323</td><td>2 April 1999 (02.04.99)</td><td>US</td></tr><tr><td>09/370,838</td><td>9 August 1999 (09.08.99)</td><td>US</td></tr><tr><td>09/476,235</td><td>30 December 1999 (30.12.99)</td><td>US</td></tr><tr><td>09/518,809</td><td>3 March 2000 (03.03.00)</td><td>US</td></tr></table> <b>(71) Applicant (for all designated States except US):</b> CORIXA CORPORATION [US/US]; Suite 200, 1124 Columbia Street, Seattle, WA 98104 (US).  <b>(72) Inventors; and</b> <b>(75) Inventors/Applicants (for US only):</b> REED, Steven, G. [US/US]; 2843 - 122nd Place NE, Bellevue, WA 98005 (US). LODES, Michael, J. [US/US]; 9223 - 36th Avenue SW, Seattle, WA 98126 (US). MOHAMATH, Raodoh [US/US]; 4205 South Morgan, Seattle, WA 98118 (US). SECRIST, Heather [US/US]; 3844 - 35th Avenue W, Seattle, WA 98199 (US).  <b>(74) Agents:</b> MAKI, David, J. et al.; Seed Intellectual Property Law Group PLLC, Suite 6300, 701 Fifth Avenue, Seattle, WA 98104-7092 (US).		09/285,323	2 April 1999 (02.04.99)	US	09/370,838	9 August 1999 (09.08.99)	US	09/476,235	30 December 1999 (30.12.99)	US	09/518,809	3 March 2000 (03.03.00)	US	<b>(81) Designated States:</b> AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).  <b>Published</b> <i>Without international search report and to be republished upon receipt of that report.</i>
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09/518,809	3 March 2000 (03.03.00)	US												
<b>(54) Title:</b> COMPOUNDS FOR THERAPY AND DIAGNOSIS OF LUNG CANCER AND METHODS FOR THEIR USE  <b>(57) Abstract</b>  Compositions and methods for the therapy and diagnosis of cancer, such as lung cancer, are disclosed. Compositions may comprise one or more lung tumor proteins, immunogenic portions thereof, or polynucleotides that encode such portions. Alternatively, a therapeutic composition may comprise an antigen presenting cell that expresses a lung tumor protein, or a T cell that is specific for cells expressing such a protein. Such compositions may be used, for example, for the prevention and treatment of diseases such as lung cancer. Diagnostic methods based on detecting a lung tumor protein, or mRNA encoding such a protein, in a sample are also provided.														

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## COMPOUNDS FOR THERAPY AND DIAGNOSIS OF LUNG CANCER AND METHODS FOR THEIR USE

### 5 TECHNICAL FIELD

The present invention relates generally to compositions and methods for the treatment of lung cancer. The invention is more specifically related to nucleotide sequences that are preferentially expressed in lung tumor tissue, together with polypeptides encoded by such nucleotide sequences. The inventive nucleotide  
10 sequences and polypeptides may be used in vaccines and pharmaceutical compositions for the treatment of lung cancer.

### BACKGROUND OF THE INVENTION

Lung cancer is the primary cause of cancer death among both men and  
15 women in the U.S., with an estimated 172,000 new cases being reported in 1994. The five-year survival rate among all lung cancer patients, regardless of the stage of disease at diagnosis, is only 13%. This contrasts with a five-year survival rate of 46% among cases detected while the disease is still localized. However, only 16% of lung cancers are discovered before the disease has spread.

20 Early detection is difficult since clinical symptoms are often not seen until the disease has reached an advanced stage. Currently, diagnosis is aided by the use of chest x-rays, analysis of the type of cells contained in sputum and fiberoptic examination of the bronchial passages. Treatment regimens are determined by the type and stage of the cancer, and include surgery, radiation therapy and/or chemotherapy. In  
25 spite of considerable research into therapies for the disease, lung cancer remains difficult to treat.

Accordingly, there remains a need in the art for improved vaccines, treatment methods and diagnostic techniques for lung cancer.

### 30 SUMMARY OF THE INVENTION

Briefly stated, the present invention provides compounds and methods

for the therapy and diagnosis of cancer, such as lung cancer. In one aspect, the present invention provides polypeptides comprising at least a portion of a lung tumor protein, or a variant thereof. Certain portions and other variants are immunogenic, such that the ability of the variant to react with antigen-specific antisera is not substantially diminished. Within certain embodiments, the polypeptide comprises a sequence that is encoded by a polynucleotide sequence selected from the group consisting of: (a) sequences recited in SEQ ID NOS: 218-222, 224-226, 249, 250, 253, 256, 266, 276, 277, 282, 285, 293, 295, 298, 299, 301, 304, 306, 316, 321, 326, 333, 336, 337, 342, 353, 359, 361, 364, 369, 372, 373, 377, 379 and 386; (b) variants of a sequence recited in SEQ ID NOS: 218-222, 224-226, 249, 250, 253, 256, 266, 276, 277, 282, 285, 293, 295, 298, 299, 301, 304, 306, 316, 321, 326, 333, 336, 337, 342, 353, 359, 361, 364, 369, 372, 373, 377, 379 and 386; and (c) complements of a sequence of (a) or (b).

The present invention further provides polynucleotides that encode a polypeptide as described above, or a portion thereof (such as a portion encoding at least 15 contiguous amino acid residues of a lung tumor protein), expression vectors comprising such polynucleotides and host cells transformed or transfected with such expression vectors.

Within other aspects, the present invention provides pharmaceutical compositions comprising a polypeptide or polynucleotide as described above and a physiologically acceptable carrier.

Within a related aspect of the present invention, vaccines are provided. Such vaccines comprise a polypeptide or polynucleotide as described above and an immunostimulant.

The present invention further provides pharmaceutical compositions that comprise: (a) an antibody or antigen-binding fragment thereof that specifically binds to a lung tumor protein; and (b) a physiologically acceptable carrier.

Within further aspects, the present invention provides pharmaceutical compositions comprising: (a) an antigen presenting cell that expresses a polypeptide as described above and (b) a pharmaceutically acceptable carrier or excipient. Antigen presenting cells include dendritic cells, macrophages, monocytes, fibroblasts and B cells.



Within related aspects, vaccines are provided that comprise: (a) an antigen presenting cell that expresses a polypeptide as described above and (b) an immunostimulant.

The present invention further provides, in other aspects, fusion proteins that comprise at least one polypeptide as described above, as well as polynucleotides encoding such fusion proteins.

Within related aspects, pharmaceutical compositions comprising a fusion protein, or a polynucleotide encoding a fusion protein, in combination with a physiologically acceptable carrier are provided.

Vaccines are further provided, within other aspects, that comprise a fusion protein, or a polynucleotide encoding a fusion protein, in combination with an immunostimulant.

Within further aspects, the present invention provides methods for inhibiting the development of a cancer in a patient, comprising administering to a patient a pharmaceutical composition or vaccine as recited above.

The present invention further provides, within other aspects, methods for removing tumor cells from a biological sample, comprising contacting a biological sample with T cells that specifically react with a lung tumor protein, wherein the step of contacting is performed under conditions and for a time sufficient to permit the removal of cells expressing the protein from the sample.

Within related aspects, methods are provided for inhibiting the development of a cancer in a patient, comprising administering to a patient a biological sample treated as described above.

Methods are further provided, within other aspects, for stimulating and/or expanding T cells specific for a lung tumor protein, comprising contacting T cells with one or more of: (i) a polypeptide as described above; (ii) a polynucleotide encoding such a polypeptide; and/or (iii) an antigen presenting cell that expresses such a polypeptide; under conditions and for a time sufficient to permit the stimulation and/or expansion of T cells. Isolated T cell populations comprising T cells prepared as described above are also provided.

Within further aspects, the present invention provides methods for

inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a T cell population as described above.

The present invention further provides methods for inhibiting the development of a cancer in a patient, comprising the steps of: (a) incubating CD4<sup>+</sup> and/or CD8<sup>+</sup> T cells isolated from a patient with one or more of: (i) a polypeptide  
5 comprising at least an immunogenic portion of a lung tumor protein; (ii) a polynucleotide encoding such a polypeptide; and (iii) an antigen-presenting cell that expressed such a polypeptide; and (b) administering to the patient an effective amount of the proliferated T cells, and thereby inhibiting the development of a cancer in the  
10 patient. Proliferated cells may, but need not, be cloned prior to administration to the patient.

Within further aspects, the present invention provides methods for determining the presence or absence of a cancer in a patient, comprising: (a) contacting a biological sample obtained from a patient with a binding agent that binds to a  
15 polypeptide as recited above; (b) detecting in the sample an amount of polypeptide that binds to the binding agent; and (c) comparing the amount of polypeptide with a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient. Within preferred embodiments, the binding agent is an antibody, more preferably a monoclonal antibody. The cancer may be lung cancer.

20 The present invention also provides, within other aspects, methods for monitoring the progression of a cancer in a patient. Such methods comprise the steps of: (a) contacting a biological sample obtained from a patient at a first point in time with a binding agent that binds to a polypeptide as recited above; (b) detecting in the sample an amount of polypeptide that binds to the binding agent; (c) repeating steps (a)  
25 and (b) using a biological sample obtained from the patient at a subsequent point in time; and (d) comparing the amount of polypeptide detected in step (c) with the amount detected in step (b) and therefrom monitoring the progression of the cancer in the patient.

The present invention further provides, within other aspects, methods for  
30 determining the presence or absence of a cancer in a patient, comprising the steps of: (a) contacting a biological sample obtained from a patient with an oligonucleotide that

hybridizes to a polynucleotide that encodes a lung tumor protein; (b) detecting in the sample a level of a polynucleotide, preferably mRNA, that hybridizes to the oligonucleotide; and (c) comparing the level of polynucleotide that hybridizes to the oligonucleotide with a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient. Within certain embodiments, the amount of mRNA is detected via polymerase chain reaction using, for example, at least one oligonucleotide primer that hybridizes to a polynucleotide encoding a polypeptide as recited above, or a complement of such a polynucleotide. Within other embodiments, the amount of mRNA is detected using a hybridization technique, employing an oligonucleotide probe that hybridizes to a polynucleotide that encodes a polypeptide as recited above, or a complement of such a polynucleotide.

In related aspects, methods are provided for monitoring the progression of a cancer in a patient, comprising the steps of: (a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide that encodes a lung tumor protein; (b) detecting in the sample an amount of a polynucleotide that hybridizes to the oligonucleotide; (c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and (d) comparing the amount of polynucleotide detected in step (c) with the amount detected in step (b) and therefrom monitoring the progression of the cancer in the patient.

Within further aspects, the present invention provides antibodies, such as monoclonal antibodies, that bind to a polypeptide as described above, as well as diagnostic kits comprising such antibodies. Diagnostic kits comprising one or more oligonucleotide probes or primers as described above are also provided.

These and other aspects of the present invention will become apparent upon reference to the following detailed description and attached drawings. All references disclosed herein are hereby incorporated by reference in their entirety as if each was incorporated individually.

#### SEQUENCE IDENTIFIERS

SEQ ID NO: 1 is the determined cDNA sequence for L363C1.cons  
SEQ ID NO: 2 is the determined cDNA sequence for L263C2.cons

- SEQ ID NO: 3 is the determined cDNA sequence for L263C2c  
SEQ ID NO: 4 is the determined cDNA sequence for L263C1.cons  
SEQ ID NO: 5 is the determined cDNA sequence for L263C1b  
SEQ ID NO: 6 is the determined cDNA sequence for L164C2.cons  
5 SEQ ID NO: 7 is the determined cDNA sequence for L164C1.cons  
SEQ ID NO: 8 is the determined cDNA sequence for L366C1a  
SEQ ID NO: 9 is the determined cDNA sequence for L260C1.cons  
SEQ ID NO: 10 is the determined cDNA sequence for L163C1c  
SEQ ID NO: 11 is the determined cDNA sequence for L163C1b  
10 SEQ ID NO: 12 is the determined cDNA sequence for L255C1.cons  
SEQ ID NO: 13 is the determined cDNA sequence for L255C1b  
SEQ ID NO: 14 is the determined cDNA sequence for L355C1.cons  
SEQ ID NO: 15 is the determined cDNA sequence for L366C1.cons  
SEQ ID NO: 16 is the determined cDNA sequence for L163C1a  
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SEQ ID NO: 18 is the determined cDNA sequence for LT86-2  
SEQ ID NO: 19 is the determined cDNA sequence for LT86-3  
SEQ ID NO: 20 is the determined cDNA sequence for LT86-4  
SEQ ID NO: 21 is the determined cDNA sequence for LT86-5  
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SEQ ID NO: 23 is the determined cDNA sequence for LT86-7  
SEQ ID NO: 24 is the determined cDNA sequence for LT86-8  
SEQ ID NO: 25 is the determined cDNA sequence for LT86-9  
SEQ ID NO: 26 is the determined cDNA sequence for LT86-10  
25 SEQ ID NO: 27 is the determined cDNA sequence for LT86-11  
SEQ ID NO: 28 is the determined cDNA sequence for LT86-12  
SEQ ID NO: 29 is the determined cDNA sequence for LT86-13  
SEQ ID NO: 30 is the determined cDNA sequence for LT86-14  
SEQ ID NO: 31 is the determined cDNA sequence for LT86-15  
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SEQ ID NO: 33 is the predicted amino acid sequence for LT86-2

- SEQ ID NO: 34 is the predicted amino acid sequence for LT86-3  
SEQ ID NO: 35 is the predicted amino acid sequence for LT86-4  
SEQ ID NO: 36 is the predicted amino acid sequence for LT86-5  
SEQ ID NO: 37 is the predicted amino acid sequence for LT86-6  
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SEQ ID NO: 39 is the predicted amino acid sequence for LT86-8  
SEQ ID NO: 40 is the predicted amino acid sequence for LT86-9  
SEQ ID NO: 41 is the predicted amino acid sequence for LT86-10  
SEQ ID NO: 42 is the predicted amino acid sequence for LT86-11  
10 SEQ ID NO: 43 is the predicted amino acid sequence for LT86-12  
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SEQ ID NO: 46 is the predicted amino acid sequence for LT86-15  
SEQ ID NO: 47 is a (dT)<sub>12</sub>AG primer  
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SEQ ID NO: 59 is the predicted amino acid sequence for L86S-25  
SEQ ID NO: 60 is the predicted amino acid sequence for L86S-36  
SEQ ID NO: 61 is the predicted amino acid sequence for L86S-40  
SEQ ID NO: 62 is the predicted amino acid sequence for L86S-46  
30 SEQ ID NO: 63 is the determined 5' cDNA sequence for L86S-30  
SEQ ID NO: 64 is the determined 5' cDNA sequence for L86S-41

- SEQ ID NO: 65 is the predicted amino acid sequence from the 5' end of LT86-9
- SEQ ID NO: 66 is the determined extended cDNA sequence for LT86-4
- SEQ ID NO: 67 is the predicted extended amino acid sequence for LT86-4
- SEQ ID NO: 68 is the determined 5' cDNA sequence for LT86-20
- 5 SEQ ID NO: 69 is the determined 3' cDNA sequence for LT86-21
- SEQ ID NO: 70 is the determined 5' cDNA sequence for LT86-22
- SEQ ID NO: 71 is the determined 5' cDNA sequence for LT86-26
- SEQ ID NO: 72 is the determined 5' cDNA sequence for LT86-27
- SEQ ID NO: 73 is the predicted amino acid sequence for LT86-20
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- SEQ ID NO: 77 is the predicted amino acid sequence for LT86-27
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- SEQ ID NO: 81 is the predicted extended amino acid sequence for L86S-12
- SEQ ID NO: 82 is the predicted extended amino acid sequence for L86S-36
- SEQ ID NO: 83 is the predicted extended amino acid sequence for L86S-46
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- SEQ ID NO: 85 is the determined 5'cDNA sequence for L86S-11
- SEQ ID NO: 86 is the determined 5'cDNA sequence for L86S-14
- SEQ ID NO: 87 is the determined 5'cDNA sequence for L86S-29
- SEQ ID NO: 88 is the determined 5'cDNA sequence for L86S-34
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- SEQ ID NO: 90 is the determined 5'cDNA sequence for L86S-47
- SEQ ID NO: 91 is the determined 5'cDNA sequence for L86S-49
- SEQ ID NO: 92 is the determined 5'cDNA sequence for L86S-51
- SEQ ID NO: 93 is the predicted amino acid sequence for L86S-6
- 30 SEQ ID NO: 94 is the predicted amino acid sequence for L86S-11
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- SEQ ID NO: 127 is the determined cDNA sequence for PSLT-2  
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- SEQ ID NO: 158 is the determined 5' cDNA sequence for SAL-104  
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SEQ ID NO: 184 is a first predicted amino acid sequence for SAL-25  
SEQ ID NO: 185 is a second predicted amino acid sequence for SAL-25  
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30 SEQ ID NO: 187 is a first predicted amino acid sequence for SAL-50  
SEQ ID NO: 188 is the predicted amino acid sequence for SAL-57

- SEQ ID NO: 189 is a first predicted amino acid sequence for SAL-66
- SEQ ID NO: 190 is a second predicted amino acid sequence for SAL-66
- SEQ ID NO: 191 is the predicted amino acid sequence for SAL-82
- SEQ ID NO: 192 is the predicted amino acid sequence for SAL-99
- 5 SEQ ID NO: 193 is the predicted amino acid sequence for SAL-104
- SEQ ID NO: 194 is the predicted amino acid sequence for SAL-5
- SEQ ID NO: 195 is the predicted amino acid sequence for SAL-8
- SEQ ID NO: 196 is the predicted amino acid sequence for SAL-12
- SEQ ID NO: 197 is the predicted amino acid sequence for SAL-14
- 10 SEQ ID NO: 198 is the predicted amino acid sequence for SAL-16
- SEQ ID NO: 199 is the predicted amino acid sequence for SAL-23
- SEQ ID NO: 200 is the predicted amino acid sequence for SAL-26
- SEQ ID NO: 201 is the predicted amino acid sequence for SAL-29
- SEQ ID NO: 202 is the predicted amino acid sequence for SAL-32
- 15 SEQ ID NO: 203 is the predicted amino acid sequence for SAL-39
- SEQ ID NO: 204 is the predicted amino acid sequence for SAL-42
- SEQ ID NO: 205 is the predicted amino acid sequence for SAL-43
- SEQ ID NO: 206 is the predicted amino acid sequence for SAL-44
- SEQ ID NO: 207 is the predicted amino acid sequence for SAL-48
- 20 SEQ ID NO: 208 is the predicted amino acid sequence for SAL-68
- SEQ ID NO: 209 is the predicted amino acid sequence for SAL-72
- SEQ ID NO: 210 is the predicted amino acid sequence for SAL-77
- SEQ ID NO: 211 is the predicted amino acid sequence for SAL-86
- SEQ ID NO: 212 is the predicted amino acid sequence for SAL-88
- 25 SEQ ID NO: 213 is the predicted amino acid sequence for SAL-93
- SEQ ID NO: 214 is the predicted amino acid sequence for SAL-100
- SEQ ID NO: 215 is the predicted amino acid sequence for SAL-105
- SEQ ID NO: 216 is a second predicted amino acid sequence for SAL-50
- SEQ ID NO: 217 is the determined cDNA sequence for SSLT-4
- 30 SEQ ID NO: 218 is the determined cDNA sequence for SSLT-9
- SEQ ID NO: 219 is the determined cDNA sequence for SSLT-10

- SEQ ID NO: 220 is the determined cDNA sequence for SSLT-12  
SEQ ID NO: 221 is the determined cDNA sequence for SSLT-19  
SEQ ID NO: 222 is the determined cDNA sequence for SSLT-31  
SEQ ID NO: 223 is the determined cDNA sequence for SSLT-38  
5 SEQ ID NO: 224 is the determined cDNA sequence for LT4690-2  
SEQ ID NO: 225 is the determined cDNA sequence for LT4690-3  
SEQ ID NO: 226 is the determined cDNA sequence for LT4690-22  
SEQ ID NO: 227 is the determined cDNA sequence for LT4690-24  
SEQ ID NO: 228 is the determined cDNA sequence for LT4690-37  
10 SEQ ID NO: 229 is the determined cDNA sequence for LT4690-39  
SEQ ID NO: 230 is the determined cDNA sequence for LT4690-40  
SEQ ID NO: 231 is the determined cDNA sequence for LT4690-41  
SEQ ID NO: 232 is the determined cDNA sequence for LT4690-49  
SEQ ID NO: 233 is the determined 3' cDNA sequence for LT4690-55  
15 SEQ ID NO: 234 is the determined 5' cDNA sequence for LT4690-55  
SEQ ID NO: 235 is the determined cDNA sequence for LT4690-59  
SEQ ID NO: 236 is the determined cDNA sequence for LT4690-63  
SEQ ID NO: 237 is the determined cDNA sequence for LT4690-71  
SEQ ID NO: 238 is the determined cDNA sequence for 2LT-3  
20 SEQ ID NO: 239 is the determined cDNA sequence for 2LT-6  
SEQ ID NO: 240 is the determined cDNA sequence for 2LT-22  
SEQ ID NO: 241 is the determined cDNA sequence for 2LT-25  
SEQ ID NO: 242 is the determined cDNA sequence for 2LT-26  
SEQ ID NO: 243 is the determined cDNA sequence for 2LT-31  
25 SEQ ID NO: 244 is the determined cDNA sequence for 2LT-36  
SEQ ID NO: 245 is the determined cDNA sequence for 2LT-42  
SEQ ID NO: 246 is the determined cDNA sequence for 2LT-44  
SEQ ID NO: 247 is the determined cDNA sequence for 2LT-54  
SEQ ID NO: 248 is the determined cDNA sequence for 2LT-55  
30 SEQ ID NO: 249 is the determined cDNA sequence for 2LT-57  
SEQ ID NO: 250 is the determined cDNA sequence for 2LT-58

- SEQ ID NO: 251 is the determined cDNA sequence for 2LT-59  
SEQ ID NO: 252 is the determined cDNA sequence for 2LT-62  
SEQ ID NO: 253 is the determined cDNA sequence for 2LT-63  
SEQ ID NO: 254 is the determined cDNA sequence for 2LT-65  
5 SEQ ID NO: 255 is the determined cDNA sequence for 2LT-66  
SEQ ID NO: 256 is the determined cDNA sequence for 2LT-70  
SEQ ID NO: 257 is the determined cDNA sequence for 2LT-73  
SEQ ID NO: 258 is the determined cDNA sequence for 2LT-74  
SEQ ID NO: 259 is the determined cDNA sequence for 2LT-76  
10 SEQ ID NO: 260 is the determined cDNA sequence for 2LT-77  
SEQ ID NO: 261 is the determined cDNA sequence for 2LT-78  
SEQ ID NO: 262 is the determined cDNA sequence for 2LT-80  
SEQ ID NO: 263 is the determined cDNA sequence for 2LT-85  
SEQ ID NO: 264 is the determined cDNA sequence for 2LT-87  
15 SEQ ID NO: 265 is the determined cDNA sequence for 2LT-89  
SEQ ID NO: 266 is the determined cDNA sequence for 2LT-94  
SEQ ID NO: 267 is the determined cDNA sequence for 2LT-95  
SEQ ID NO: 268 is the determined cDNA sequence for 2LT-98  
SEQ ID NO: 269 is the determined cDNA sequence for 2LT-100  
20 SEQ ID NO: 270 is the determined cDNA sequence for 2LT-103  
SEQ ID NO: 271 is the determined cDNA sequence for 2LT-105  
SEQ ID NO: 272 is the determined cDNA sequence for 2LT-107  
SEQ ID NO: 273 is the determined cDNA sequence for 2LT-108  
SEQ ID NO: 274 is the determined cDNA sequence for 2LT-109  
25 SEQ ID NO: 275 is the determined cDNA sequence for 2LT-118  
SEQ ID NO: 276 is the determined cDNA sequence for 2LT-120  
SEQ ID NO: 277 is the determined cDNA sequence for 2LT-121  
SEQ ID NO: 278 is the determined cDNA sequence for 2LT-122  
SEQ ID NO: 279 is the determined cDNA sequence for 2LT-124  
30 SEQ ID NO: 280 is the determined cDNA sequence for 2LT-126  
SEQ ID NO: 281 is the determined cDNA sequence for 2LT-127

- SEQ ID NO: 282 is the determined cDNA sequence for 2LT-128  
SEQ ID NO: 283 is the determined cDNA sequence for 2LT-129  
SEQ ID NO: 284 is the determined cDNA sequence for 2LT-133  
SEQ ID NO: 285 is the determined cDNA sequence for 2LT-137  
5 SEQ ID NO: 286 is the determined cDNA sequence for LT4690-71  
SEQ ID NO: 287 is the determined cDNA sequence for LT4690-82  
SEQ ID NO: 288 is the determined full-length cDNA sequence for SSLT-74  
SEQ ID NO: 289 is the determined cDNA sequence for SSLT-78  
SEQ ID NO: 290 is the determined cDNA sequence for SCC1-8.  
10 SEQ ID NO: 291 is the determined cDNA sequence for SCC1-12.  
SEQ ID NO: 292 is the determined cDNA sequence for SCC1-336  
SEQ ID NO: 293 is the determined cDNA sequence for SCC1-344  
SEQ ID NO: 294 is the determined cDNA sequence for SCC1-345  
SEQ ID NO: 295 is the determined cDNA sequence for SCC1-346  
15 SEQ ID NO: 296 is the determined cDNA sequence for SCC1-348  
SEQ ID NO: 297 is the determined cDNA sequence for SCC1-350  
SEQ ID NO: 298 is the determined cDNA sequence for SCC1-352  
SEQ ID NO: 299 is the determined cDNA sequence for SCC1-354  
SEQ ID NO: 300 is the determined cDNA sequence for SCC1-355  
20 SEQ ID NO: 301 is the determined cDNA sequence for SCC1-356  
SEQ ID NO: 302 is the determined cDNA sequence for SCC1-357  
SEQ ID NO: 303 is the determined cDNA sequence for SCC1-501  
SEQ ID NO: 304 is the determined cDNA sequence for SCC1-503  
SEQ ID NO: 305 is the determined cDNA sequence for SCC1-513  
25 SEQ ID NO: 306 is the determined cDNA sequence for SCC1-516  
SEQ ID NO: 307 is the determined cDNA sequence for SCC1-518  
SEQ ID NO: 308 is the determined cDNA sequence for SCC1-519  
SEQ ID NO: 309 is the determined cDNA sequence for SCC1-522  
SEQ ID NO: 310 is the determined cDNA sequence for SCC1-523  
30 SEQ ID NO: 311 is the determined cDNA sequence for SCC1-525  
SEQ ID NO: 312 is the determined cDNA sequence for SCC1-527



- SEQ ID NO: 313 is the determined cDNA sequence for SCC1-529  
SEQ ID NO: 314 is the determined cDNA sequence for SCC1-530  
SEQ ID NO: 315 is the determined cDNA sequence for SCC1-531  
SEQ ID NO: 316 is the determined cDNA sequence for SCC1-532  
5 SEQ ID NO: 317 is the determined cDNA sequence for SCC1-533  
SEQ ID NO: 318 is the determined cDNA sequence for SCC1-536  
SEQ ID NO: 319 is the determined cDNA sequence for SCC1-538  
SEQ ID NO: 320 is the determined cDNA sequence for SCC1-539  
SEQ ID NO: 321 is the determined cDNA sequence for SCC1-541  
10 SEQ ID NO: 322 is the determined cDNA sequence for SCC1-542  
SEQ ID NO: 323 is the determined cDNA sequence for SCC1-546  
SEQ ID NO: 324 is the determined cDNA sequence for SCC1-549  
SEQ ID NO: 325 is the determined cDNA sequence for SCC1-551  
SEQ ID NO: 326 is the determined cDNA sequence for SCC1-552  
15 SEQ ID NO: 327 is the determined cDNA sequence for SCC1-554  
SEQ ID NO: 328 is the determined cDNA sequence for SCC1-558  
SEQ ID NO: 329 is the determined cDNA sequence for SCC1-559  
SEQ ID NO: 330 is the determined cDNA sequence for SCC1-561  
SEQ ID NO: 331 is the determined cDNA sequence for SCC1-562  
20 SEQ ID NO: 332 is the determined cDNA sequence for SCC1-564  
SEQ ID NO: 333 is the determined cDNA sequence for SCC1-565  
SEQ ID NO: 334 is the determined cDNA sequence for SCC1-566  
SEQ ID NO: 335 is the determined cDNA sequence for SCC1-567  
SEQ ID NO: 336 is the determined cDNA sequence for SCC1-568  
25 SEQ ID NO: 337 is the determined cDNA sequence for SCC1-570  
SEQ ID NO: 338 is the determined cDNA sequence for SCC1-572  
SEQ ID NO: 339 is the determined cDNA sequence for SCC1-575  
SEQ ID NO: 340 is the determined cDNA sequence for SCC1-576  
SEQ ID NO: 341 is the determined cDNA sequence for SCC1-577  
30 SEQ ID NO: 342 is the determined cDNA sequence for SCC1-578  
SEQ ID NO: 343 is the determined cDNA sequence for SCC1-582



- SEQ ID NO: 344 is the determined cDNA sequence for SCC1-583  
SEQ ID NO: 345 is the determined cDNA sequence for SCC1-586  
SEQ ID NO: 346 is the determined cDNA sequence for SCC1-588  
SEQ ID NO: 347 is the determined cDNA sequence for SCC1-590  
5 SEQ ID NO: 348 is the determined cDNA sequence for SCC1-591  
SEQ ID NO: 349 is the determined cDNA sequence for SCC1-592  
SEQ ID NO: 350 is the determined cDNA sequence for SCC1-593  
SEQ ID NO: 351 is the determined cDNA sequence for SCC1-594  
SEQ ID NO: 352 is the determined cDNA sequence for SCC1-595  
10 SEQ ID NO: 353 is the determined cDNA sequence for SCC1-596  
SEQ ID NO: 354 is the determined cDNA sequence for SCC1-598  
SEQ ID NO: 355 is the determined cDNA sequence for SCC1-599  
SEQ ID NO: 356 is the determined cDNA sequence for SCC1-602  
SEQ ID NO: 357 is the determined cDNA sequence for SCC1-604  
15 SEQ ID NO: 358 is the determined cDNA sequence for SCC1-605  
SEQ ID NO: 359 is the determined cDNA sequence for SCC1-606  
SEQ ID NO: 360 is the determined cDNA sequence for SCC1-607  
SEQ ID NO: 361 is the determined cDNA sequence for SCC1-608  
SEQ ID NO: 362 is the determined cDNA sequence for SCC1-610  
20 SEQ ID NO: 363 is the determined cDNA sequence for clone DMS79T1  
SEQ ID NO: 364 is the determined cDNA sequence for clone DMS79T2  
SEQ ID NO: 365 is the determined cDNA sequence for clone DMS79T3  
SEQ ID NO: 366 is the determined cDNA sequence for clone DMS79T5  
SEQ ID NO: 367 is the determined cDNA sequence for clone DMS79T6  
25 SEQ ID NO: 368 is the determined cDNA sequence for clone DMS79T7  
SEQ ID NO: 369 is the determined cDNA sequence for clone DMS79T9  
SEQ ID NO: 370 is the determined cDNA sequence for clone DMS79T10  
SEQ ID NO: 371 is the determined cDNA sequence for clone DMS79T11  
SEQ ID NO: 372 is the determined cDNA sequence for clone 128T1  
30 SEQ ID NO: 373 is the determined cDNA sequence for clone 128T2  
SEQ ID NO: 374 is the determined cDNA sequence for clone 128T3

- SEQ ID NO: 375 is the determined cDNA sequence for clone 128T4  
SEQ ID NO: 376 is the determined cDNA sequence for clone 128T5  
SEQ ID NO: 377 is the determined cDNA sequence for clone 128T7  
SEQ ID NO: 378 is the determined cDNA sequence for clone 128T9  
5 SEQ ID NO: 379 is the determined cDNA sequence for clone 128T10  
SEQ ID NO: 380 is the determined cDNA sequence for clone 128T11  
SEQ ID NO: 381 is the determined cDNA sequence for clone 128T12  
SEQ ID NO: 382 is the determined cDNA sequence for clone NCIH69T3  
SEQ ID NO: 383 is the determined cDNA sequence for clone NCIH69T5  
10 SEQ ID NO: 384 is the determined cDNA sequence for clone NCIH69T6  
SEQ ID NO: 385 is the determined cDNA sequence for clone NCIH69T7  
SEQ ID NO: 386 is the determined cDNA sequence for clone NCIH69T9  
SEQ ID NO: 387 is the determined cDNA sequence for clone NCIH69T10  
SEQ ID NO: 388 is the determined cDNA sequence for clone NCIH69T11  
15 SEQ ID NO: 389 is the determined cDNA sequence for clone NCIH69T12

#### DETAILED DESCRIPTION OF THE INVENTION

- As noted above, the present invention is generally directed to compositions and methods for the therapy and diagnosis of cancer, such as lung cancer.
- 20 The compositions described herein may include lung tumor polypeptides, polynucleotides encoding such polypeptides, binding agents such as antibodies, antigen presenting cells (APCs) and/or immune system cells (*e.g.*, T cells). Polypeptides of the present invention generally comprise at least a portion (such as an immunogenic portion) of a lung tumor protein or a variant thereof. A "lung tumor protein" is a protein
- 25 that is expressed in lung tumor cells at a level that is at least two fold, and preferably at least five fold, greater than the level of expression in a normal tissue, as determined using a representative assay provided herein. Certain lung tumor proteins are tumor proteins that react detectably (within an immunoassay, such as an ELISA or Western blot) with antisera of a patient afflicted with lung cancer. Polynucleotides of the subject
- 30 invention generally comprise a DNA or RNA sequence that encodes all or a portion of such a polypeptide, or that is complementary to such a sequence. Antibodies are

generally immune system proteins, or antigen-binding fragments thereof, that are capable of binding to a polypeptide as described above. Antigen presenting cells include dendritic cells, macrophages, monocytes, fibroblasts and B-cells that express a polypeptide as described above. T cells that may be employed within such compositions are generally T cells that are specific for a polypeptide as described above.

The present invention is based on the discovery of human lung tumor proteins. Sequences of polynucleotides encoding specific tumor proteins are provided in SEQ ID NOS: 1-31, 49-55, 63,64, 66, 68-72, 78-80, 84-92 and 217-389.

#### LUNG TUMOR PROTEIN POLYNUCLEOTIDES

Any polynucleotide that encodes a lung tumor protein or a portion or other variant thereof as described herein is encompassed by the present invention. Preferred polynucleotides comprise at least 15 consecutive nucleotides, preferably at least 30 consecutive nucleotides and more preferably at least 45 consecutive nucleotides, that encode a portion of a lung tumor protein. More preferably, a polynucleotide encodes an immunogenic portion of a lung tumor protein. Polynucleotides complementary to any such sequences are also encompassed by the present invention. Polynucleotides may be single-stranded (coding or antisense) or double-stranded, and may be DNA (genomic, cDNA or synthetic) or RNA molecules. RNA molecules include HnRNA molecules, which contain introns and correspond to a DNA molecule in a one-to-one manner, and mRNA molecules, which do not contain introns. Additional coding or non-coding sequences may, but need not, be present within a polynucleotide of the present invention, and a polynucleotide may, but need not, be linked to other molecules and/or support materials.

Polynucleotides may comprise a native sequence (*i.e.*, an endogenous sequence that encodes a lung tumor protein or a portion thereof) or may comprise a variant of such a sequence. Polynucleotide variants may contain one or more substitutions, additions, deletions and/or insertions such that the immunogenicity of the encoded polypeptide is not diminished, relative to a native tumor protein. The effect on the immunogenicity of the encoded polypeptide may generally be assessed as described

herein. Variants preferably exhibit at least about 70% identity, more preferably at least about 80% identity and most preferably at least about 90% identity to a polynucleotide sequence that encodes a native lung tumor protein or a portion thereof.

Two polynucleotide or polypeptide sequences are said to be "identical" if  
5 the sequence of nucleotides or amino acids in the two sequences is the same when aligned for maximum correspondence as described below. Comparisons between two sequences are typically performed by comparing the sequences over a comparison window to identify and compare local regions of sequence similarity. A "comparison window" as used herein, refers to a segment of at least about 20 contiguous positions,  
10 usually 30 to about 75, 40 to about 50, in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned.

Optimal alignment of sequences for comparison may be conducted using the Megalign program in the Lasergene suite of bioinformatics software (DNASTAR, Inc., Madison, WI), using default parameters. This program embodies several  
15 alignment schemes described in the following references: Dayhoff, M.O. (1978) A model of evolutionary change in proteins – Matrices for detecting distant relationships. In Dayhoff, M.O. (ed.) Atlas of Protein Sequence and Structure, National Biomedical Research Foundation, Washington DC Vol. 5, Suppl. 3, pp. 345-358; Hein J. (1990) Unified Approach to Alignment and Phylogenesis pp. 626-645 *Methods in Enzymology*  
20 vol. 183, Academic Press, Inc., San Diego, CA; Higgins, D.G. and Sharp, P.M. (1989) *CABIOS* 5:151-153; Myers, E.W. and Muller W. (1988) *CABIOS* 4:11-17; Robinson, E.D. (1971) *Comb. Theor* 11:105; Santou, N. Nes, M. (1987) *Mol. Biol. Evol.* 4:406-425; Sneath, P.H.A. and Sokal, R.R. (1973) *Numerical Taxonomy – the Principles and Practice of Numerical Taxonomy*, Freeman Press, San Francisco, CA; Wilbur, W.J. and  
25 Lipman, D.J. (1983) *Proc. Natl. Acad., Sci. USA* 80:726-730.

Preferably, the "percentage of sequence identity" is determined by comparing two optimally aligned sequences over a window of comparison of at least 20 positions, wherein the portion of the polynucleotide or polypeptide sequence in the  
30 comparison window may comprise additions or deletions (i.e. gaps) of 20 percent or less, usually 5 to 15 percent, or 10 to 12 percent, as compared to the reference

sequences (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid bases or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the reference sequence (i.e. the window size) and multiplying the results by 100 to yield the percentage of sequence identity.

Variants may also, or alternatively, be substantially homologous to a native gene, or a portion or complement thereof. Such polynucleotide variants are capable of hybridizing under moderately stringent conditions to a naturally occurring DNA sequence encoding a native lung tumor protein (or a complementary sequence). Suitable moderately stringent conditions include prewashing in a solution of 5 X SSC, 0.5% SDS, 1.0 mM EDTA (pH 8.0); hybridizing at 50°C-65°C, 5 X SSC, overnight; followed by washing twice at 65°C for 20 minutes with each of 2X, 0.5X and 0.2X SSC containing 0.1% SDS.

It will be appreciated by those of ordinary skill in the art that, as a result of the degeneracy of the genetic code, there are many nucleotide sequences that encode a polypeptide as described herein. Some of these polynucleotides bear minimal homology to the nucleotide sequence of any native gene. Nonetheless, polynucleotides that vary due to differences in codon usage are specifically contemplated by the present invention. Further, alleles of the genes comprising the polynucleotide sequences provided herein are within the scope of the present invention. Alleles are endogenous genes that are altered as a result of one or more mutations, such as deletions, additions and/or substitutions of nucleotides. The resulting mRNA and protein may, but need not, have an altered structure or function. Alleles may be identified using standard techniques (such as hybridization, amplification and/or database sequence comparison).

Polynucleotides may be prepared using any of a variety of techniques. For example, a polynucleotide may be identified, as described in more detail below, by screening a microarray of cDNAs for tumor-associated expression (*i.e.*, expression that is at least five fold greater in a lung tumor than in normal tissue, as determined using a representative assay provided herein). Such screens may be performed using a Synteni microarray (Palo Alto, CA) according to the manufacturer's instructions (and essentially

as described by Schena et al., *Proc. Natl. Acad. Sci. USA* 93:10614-10619, 1996 and Heller et al., *Proc. Natl. Acad. Sci. USA* 94:2150-2155, 1997). Alternatively, polypeptides may be amplified from cDNA prepared from cells expressing the proteins described herein, such as lung tumor cells. Such polynucleotides may be amplified via  
5 polymerase chain reaction (PCR). For this approach, sequence-specific primers may be designed based on the sequences provided herein, and may be purchased or synthesized.

An amplified portion may be used to isolate a full length gene from a suitable library (e.g., a lung tumor cDNA library) using well known techniques. Within such techniques, a library (cDNA or genomic) is screened using one or more  
10 polynucleotide probes or primers suitable for amplification. Preferably, a library is size-selected to include larger molecules. Random primed libraries may also be preferred for identifying 5' and upstream regions of genes. Genomic libraries are preferred for obtaining introns and extending 5' sequences.

For hybridization techniques, a partial sequence may be labeled (e.g., by  
15 nick-translation or end-labeling with  $^{32}\text{P}$ ) using well known techniques. A bacterial or bacteriophage library is then screened by hybridizing filters containing denatured bacterial colonies (or lawns containing phage plaques) with the labeled probe (see Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratories, Cold Spring Harbor, NY, 1989). Hybridizing colonies or plaques are  
20 selected and expanded, and the DNA is isolated for further analysis. cDNA clones may be analyzed to determine the amount of additional sequence by, for example, PCR using a primer from the partial sequence and a primer from the vector. Restriction maps and partial sequences may be generated to identify one or more overlapping clones. The complete sequence may then be determined using standard techniques, which may  
25 involve generating a series of deletion clones. The resulting overlapping sequences are then assembled into a single contiguous sequence. A full length cDNA molecule can be generated by ligating suitable fragments, using well known techniques.

Alternatively, there are numerous amplification techniques for obtaining a full length coding sequence from a partial cDNA sequence. Within such techniques,  
30 amplification is generally performed via PCR. Any of a variety of commercially available kits may be used to perform the amplification step. Primers may be designed



using, for example, software well known in the art. Primers are preferably 22-30 nucleotides in length, have a GC content of at least 50% and anneal to the target sequence at temperatures of about 68°C to 72°C. The amplified region may be sequenced as described above, and overlapping sequences assembled into a contiguous  
5 sequence.

One such amplification technique is inverse PCR (*see* Triglia et al., *Nucl. Acids Res.* 16:8186, 1988), which uses restriction enzymes to generate a fragment in the known region of the gene. The fragment is then circularized by intramolecular ligation and used as a template for PCR with divergent primers derived from the known region.  
10 Within an alternative approach, sequences adjacent to a partial sequence may be retrieved by amplification with a primer to a linker sequence and a primer specific to a known region. The amplified sequences are typically subjected to a second round of amplification with the same linker primer and a second primer specific to the known region. A variation on this procedure, which employs two primers that initiate  
15 extension in opposite directions from the known sequence, is described in WO 96/38591. Another such technique is known as "rapid amplification of cDNA ends" or RACE. This technique involves the use of an internal primer and an external primer, which hybridizes to a polyA region or vector sequence, to identify sequences that are 5' and 3' of a known sequence. Additional techniques include capture PCR (Lagerstrom et  
20 al., *PCR Methods Applic.* 1:111-19, 1991) and walking PCR (Parker et al., *Nucl. Acids Res.* 19:3055-60, 1991). Other methods employing amplification may also be employed to obtain a full length cDNA sequence.

In certain instances, it is possible to obtain a full length cDNA sequence by analysis of sequences provided in an expressed sequence tag (EST) database, such as  
25 that available from GenBank. Searches for overlapping ESTs may generally be performed using well known programs (*e.g.*, NCBI BLAST searches), and such ESTs may be used to generate a contiguous full length sequence.

Certain nucleic acid sequences of cDNA molecules encoding portions of lung tumor proteins are provided in SEQ ID NO: 1-31, 49-55, 63,64, 66, 68-72, 78-80,  
30 84-92 and 217-389. The isolation of these sequences is described in detail below.

Polynucleotide variants may generally be prepared by any method



known in the art, including chemical synthesis by, for example, solid phase phosphoramidite chemical synthesis. Modifications in a polynucleotide sequence may also be introduced using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis (*see* Adelman et al., *DNA* 2:183, 1983).

5 Alternatively, RNA molecules may be generated by *in vitro* or *in vivo* transcription of DNA sequences encoding a lung tumor protein, or portion thereof, provided that the DNA is incorporated into a vector with a suitable RNA polymerase promoter (such as T7 or SP6). Certain portions may be used to prepare an encoded polypeptide, as described herein. In addition, or alternatively, a portion may be administered to a

10 patient such that the encoded polypeptide is generated *in vivo* (*e.g.*, by transfecting antigen-presenting cells, such as dendritic cells, with a cDNA construct encoding a lung tumor polypeptide, and administering the transfected cells to the patient).

A portion of a sequence complementary to a coding sequence (*i.e.*, an antisense polynucleotide) may also be used as a probe or to modulate gene expression.

15 cDNA constructs that can be transcribed into antisense RNA may also be introduced into cells of tissues to facilitate the production of antisense RNA. An antisense polynucleotide may be used, as described herein, to inhibit expression of a tumor protein. Antisense technology can be used to control gene expression through triple-helix formation, which compromises the ability of the double helix to open sufficiently

20 for the binding of polymerases, transcription factors or regulatory molecules (*see* Gee et al., *In* Huber and Carr, *Molecular and Immunologic Approaches*, Futura Publishing Co. (Mt. Kisco, NY; 1994)). Alternatively, an antisense molecule may be designed to hybridize with a control region of a gene (*e.g.*, promoter, enhancer or transcription initiation site), and block transcription of the gene; or to block translation by inhibiting

25 binding of a transcript to ribosomes.

A portion of a coding sequence, or of a complementary sequence, may also be designed as a probe or primer to detect gene expression. Probes may be labeled with a variety of reporter groups, such as radionuclides and enzymes, and are preferably at least 10 nucleotides in length, more preferably at least 20 nucleotides in length and

30 still more preferably at least 30 nucleotides in length. Primers, as noted above, are preferably 22-30 nucleotides in length.

Any polynucleotide may be further modified to increase stability *in vivo*. Possible modifications include, but are not limited to, the addition of flanking sequences at the 5' and/or 3' ends; the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase linkages in the backbone; and/or the inclusion of nontraditional  
5 bases such as inosine, queosine and wybutosine, as well as acetyl-, methyl-, thio- and other modified forms of adenine, cytidine, guanine, thymine and uridine.

Nucleotide sequences as described herein may be joined to a variety of other nucleotide sequences using established recombinant DNA techniques. For example, a polynucleotide may be cloned into any of a variety of cloning vectors,  
10 including plasmids, phagemids, lambda phage derivatives and cosmids. Vectors of particular interest include expression vectors, replication vectors, probe generation vectors and sequencing vectors. In general, a vector will contain an origin of replication functional in at least one organism, convenient restriction endonuclease sites and one or more selectable markers. Other elements will depend upon the desired use, and will be  
15 apparent to those of ordinary skill in the art.

Within certain embodiments, polynucleotides may be formulated so as to permit entry into a cell of a mammal, and expression therein. Such formulations are particularly useful for therapeutic purposes, as described below. Those of ordinary skill in the art will appreciate that there are many ways to achieve expression of a  
20 polynucleotide in a target cell, and any suitable method may be employed. For example, a polynucleotide may be incorporated into a viral vector such as, but not limited to, adenovirus, adeno-associated virus, retrovirus, or vaccinia or other pox virus (*e.g.*, avian pox virus). Techniques for incorporating DNA into such vectors are well known to those of ordinary skill in the art. A retroviral vector may additionally transfer  
25 or incorporate a gene for a selectable marker (to aid in the identification or selection of transduced cells) and/or a targeting moiety, such as a gene that encodes a ligand for a receptor on a specific target cell, to render the vector target specific. Targeting may also be accomplished using an antibody, by methods known to those of ordinary skill in the art.

30 Other formulations for therapeutic purposes include colloidal dispersion systems, such as macromolecule complexes, nanocapsules, microspheres, beads, and

lipid-based systems including oil-in-water emulsions, micelles, mixed micelles, and liposomes. A preferred colloidal system for use as a delivery vehicle *in vitro* and *in vivo* is a liposome (*i.e.*, an artificial membrane vesicle). The preparation and use of such systems is well known in the art.

5

#### LUNG TUMOR POLYPEPTIDES

Within the context of the present invention, polypeptides may comprise at least an immunogenic portion of a lung tumor protein or a variant thereof, as described herein. As noted above, a "lung tumor protein" is a protein that is expressed  
10 by lung tumor cells. Proteins that are lung tumor proteins also react detectably within an immunoassay (such as an ELISA) with antisera from a patient with lung cancer. Polypeptides as described herein may be of any length. Additional sequences derived from the native protein and/or heterologous sequences may be present, and such sequences may (but need not) possess further immunogenic or antigenic properties.

15 An "immunogenic portion," as used herein is a portion of a protein that is recognized (*i.e.*, specifically bound) by a B-cell and/or T-cell surface antigen receptor. Such immunogenic portions generally comprise at least 5 amino acid residues, more preferably at least 10, and still more preferably at least 20 amino acid residues of a lung tumor protein or a variant thereof. Certain preferred immunogenic  
20 portions include peptides in which an N-terminal leader sequence and/or transmembrane domain have been deleted. Other preferred immunogenic portions may contain a small N- and/or C-terminal deletion (*e.g.*, 1-30 amino acids, preferably 5-15 amino acids), relative to the mature protein.

Immunogenic portions may generally be identified using well known  
25 techniques, such as those summarized in Paul, *Fundamental Immunology*, 3rd ed., 243-247 (Raven Press, 1993) and references cited therein. Such techniques include screening polypeptides for the ability to react with antigen-specific antibodies, antisera and/or T-cell lines or clones. As used herein, antisera and antibodies are "antigen-specific" if they specifically bind to an antigen (*i.e.*, they react with the protein in an  
30 ELISA or other immunoassay, and do not react detectably with unrelated proteins). Such antisera and antibodies may be prepared as described herein, and using well

known techniques. An immunogenic portion of a native lung tumor protein is a portion that reacts with such antisera and/or T-cells at a level that is not substantially less than the reactivity of the full length polypeptide (*e.g.*, in an ELISA and/or T-cell reactivity assay). Such immunogenic portions may react within such assays at a level that is similar to or greater than the reactivity of the full length polypeptide. Such screens may generally be performed using methods well known to those of ordinary skill in the art, such as those described in Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. For example, a polypeptide may be immobilized on a solid support and contacted with patient sera to allow binding of antibodies within the sera to the immobilized polypeptide. Unbound sera may then be removed and bound antibodies detected using, for example, <sup>125</sup>I-labeled Protein A.

As noted above, a composition may comprise a variant of a native lung tumor protein. A polypeptide "variant," as used herein, is a polypeptide that differs from a native lung tumor protein in one or more substitutions, deletions, additions and/or insertions, such that the immunogenicity of the polypeptide is not substantially diminished. In other words, the ability of a variant to react with antigen-specific antisera may be enhanced or unchanged, relative to the native protein, or may be diminished by less than 50%, and preferably less than 20%, relative to the native protein. Such variants may generally be identified by modifying one of the above polypeptide sequences and evaluating the reactivity of the modified polypeptide with antigen-specific antibodies or antisera as described herein. Preferred variants include those in which one or more portions, such as an N-terminal leader sequence or transmembrane domain, have been removed. Other preferred variants include variants in which a small portion (*e.g.*, 1-30 amino acids, preferably 5-15 amino acids) has been removed from the N- and/or C-terminal of the mature protein.

Polypeptide variants preferably exhibit at least about 70%, more preferably at least about 90% and most preferably at least about 95% identity (determined as described above) to the identified polypeptides.

Preferably, a variant contains conservative substitutions. A "conservative substitution" is one in which an amino acid is substituted for another amino acid that has similar properties, such that one skilled in the art of peptide

chemistry would expect the secondary structure and hydropathic nature of the polypeptide to be substantially unchanged. Amino acid substitutions may generally be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity and/or the amphipathic nature of the residues. For example, negatively charged amino acids include aspartic acid and glutamic acid; positively charged amino acids include lysine and arginine; and amino acids with uncharged polar head groups having similar hydrophilicity values include leucine, isoleucine and valine; glycine and alanine; asparagine and glutamine; and serine, threonine, phenylalanine and tyrosine. Other groups of amino acids that may represent conservative changes include: (1) ala, pro, gly, glu, asp, gln, asn, ser, thr; (2) cys, ser, tyr, thr; (3) val, ile, leu, met, ala, phe; (4) lys, arg, his; and (5) phe, tyr, trp, his. A variant may also, or alternatively, contain nonconservative changes. In a preferred embodiment, variant polypeptides differ from a native sequence by substitution, deletion or addition of five amino acids or fewer. Variants may also (or alternatively) be modified by, for example, the deletion or addition of amino acids that have minimal influence on the immunogenicity, secondary structure and hydropathic nature of the polypeptide.

As noted above, polypeptides may comprise a signal (or leader) sequence at the N-terminal end of the protein which co-translationally or post-translationally directs transfer of the protein. The polypeptide may also be conjugated to a linker or other sequence for ease of synthesis, purification or identification of the polypeptide (*e.g.*, poly-His), or to enhance binding of the polypeptide to a solid support. For example, a polypeptide may be conjugated to an immunoglobulin Fc region.

Polypeptides may be prepared using any of a variety of well known techniques. Recombinant polypeptides encoded by DNA sequences as described above may be readily prepared from the DNA sequences using any of a variety of expression vectors known to those of ordinary skill in the art. Expression may be achieved in any appropriate host cell that has been transformed or transfected with an expression vector containing a DNA molecule that encodes a recombinant polypeptide. Suitable host cells include prokaryotes, yeast and higher eukaryotic cells. Preferably, the host cells employed are *E. coli*, yeast or a mammalian cell line such as COS or CHO. Supernatants from suitable host/vector systems which secrete recombinant protein or



polypeptide into culture media may be first concentrated using a commercially available filter. Following concentration, the concentrate may be applied to a suitable purification matrix such as an affinity matrix or an ion exchange resin. Finally, one or more reverse phase HPLC steps can be employed to further purify a recombinant polypeptide.

Portions and other variants having fewer than about 100 amino acids, and generally fewer than about 50 amino acids, may also be generated by synthetic means, using techniques well known to those of ordinary skill in the art. For example, such polypeptides may be synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a growing amino acid chain. See Merrifield, *J. Am. Chem. Soc.* 85:2149-2146, 1963. Equipment for automated synthesis of polypeptides is commercially available from suppliers such as Perkin Elmer/Applied BioSystems Division (Foster City, CA), and may be operated according to the manufacturer's instructions.

Within certain specific embodiments, a polypeptide may be a fusion protein that comprises multiple polypeptides as described herein, or that comprises at least one polypeptide as described herein and an unrelated sequence, such as a known tumor protein. A fusion partner may, for example, assist in providing T helper epitopes (an immunological fusion partner), preferably T helper epitopes recognized by humans, or may assist in expressing the protein (an expression enhancer) at higher yields than the native recombinant protein. Certain preferred fusion partners are both immunological and expression enhancing fusion partners. Other fusion partners may be selected so as to increase the solubility of the protein or to enable the protein to be targeted to desired intracellular compartments. Still further fusion partners include affinity tags, which facilitate purification of the protein.

Fusion proteins may generally be prepared using standard techniques, including chemical conjugation. Preferably, a fusion protein is expressed as a recombinant protein, allowing the production of increased levels, relative to a non-fused protein, in an expression system. Briefly, DNA sequences encoding the polypeptide components may be assembled separately, and ligated into an appropriate expression

vector. The 3' end of the DNA sequence encoding one polypeptide component is ligated, with or without a peptide linker, to the 5' end of a DNA sequence encoding the second polypeptide component so that the reading frames of the sequences are in phase. This permits translation into a single fusion protein that retains the biological activity of both component polypeptides.

A peptide linker sequence may be employed to separate the first and the second polypeptide components by a distance sufficient to ensure that each polypeptide folds into its secondary and tertiary structures. Such a peptide linker sequence is incorporated into the fusion protein using standard techniques well known in the art. Suitable peptide linker sequences may be chosen based on the following factors: (1) their ability to adopt a flexible extended conformation; (2) their inability to adopt a secondary structure that could interact with functional epitopes on the first and second polypeptides; and (3) the lack of hydrophobic or charged residues that might react with the polypeptide functional epitopes. Preferred peptide linker sequences contain Gly, Asn and Ser residues. Other near neutral amino acids, such as Thr and Ala may also be used in the linker sequence. Amino acid sequences which may be usefully employed as linkers include those disclosed in Maratea et al., *Gene* 40:39-46, 1985; Murphy et al., *Proc. Natl. Acad. Sci. USA* 83:8258-8262, 1986; U.S. Patent No. 4,935,233 and U.S. Patent No. 4,751,180. The linker sequence may generally be from 1 to about 50 amino acids in length. Linker sequences are not required when the first and second polypeptides have non-essential N-terminal amino acid regions that can be used to separate the functional domains and prevent steric interference.

The ligated DNA sequences are operably linked to suitable transcriptional or translational regulatory elements. The regulatory elements responsible for expression of DNA are located only 5' to the DNA sequence encoding the first polypeptides. Similarly, stop codons required to end translation and transcription termination signals are only present 3' to the DNA sequence encoding the second polypeptide.

Fusion proteins are also provided that comprise a polypeptide of the present invention together with an unrelated immunogenic protein. Preferably the immunogenic protein is capable of eliciting a recall response. Examples of such



proteins include tetanus, tuberculosis and hepatitis proteins (*see, for example, Stoute et al. New Engl. J. Med., 336:86-91, 1997*).

Within preferred embodiments, an immunological fusion partner is derived from protein D, a surface protein of the gram-negative bacterium *Haemophilus influenza B* (WO 91/18926). Preferably, a protein D derivative comprises approximately the first third of the protein (*e.g.*, the first N-terminal 100-110 amino acids), and a protein D derivative may be lipidated. Within certain preferred embodiments, the first 109 residues of a Lipoprotein D fusion partner is included on the N-terminus to provide the polypeptide with additional exogenous T-cell epitopes and to increase the expression level in *E. coli* (thus functioning as an expression enhancer). The lipid tail ensures optimal presentation of the antigen to antigen presenting cells. Other fusion partners include the non-structural protein from influenzae virus, NS1 (hemagglutinin). Typically, the N-terminal 81 amino acids are used, although different fragments that include T-helper epitopes may be used.

In another embodiment, the immunological fusion partner is the protein known as LYTA, or a portion thereof (preferably a C-terminal portion). LYTA is derived from *Streptococcus pneumoniae*, which synthesizes an N-acetyl-L-alanine amidase known as amidase LYTA (encoded by the *LytA* gene; *Gene* 43:265-292, 1986). LYTA is an autolysin that specifically degrades certain bonds in the peptidoglycan backbone. The C-terminal domain of the LYTA protein is responsible for the affinity to the choline or to some choline analogues such as DEAE. This property has been exploited for the development of *E. coli* C-LYTA expressing plasmids useful for expression of fusion proteins. Purification of hybrid proteins containing the C-LYTA fragment at the amino terminus has been described (*see Biotechnology* 10:795-798, 1992). Within a preferred embodiment, a repeat portion of LYTA may be incorporated into a fusion protein. A repeat portion is found in the C-terminal region starting at residue 178. A particularly preferred repeat portion incorporates residues 188-305.

In general, polypeptides (including fusion proteins) and polynucleotides as described herein are isolated. An "isolated" polypeptide or polynucleotide is one that is removed from its original environment. For example, a naturally-occurring protein is

isolated if it is separated from some or all of the coexisting materials in the natural system. Preferably, such polypeptides are at least about 90% pure, more preferably at least about 95% pure and most preferably at least about 99% pure. A polynucleotide is considered to be isolated if, for example, it is cloned into a vector that is not a part of  
5 the natural environment.

#### BINDING AGENTS

The present invention further provides agents, such as antibodies and antigen-binding fragments thereof, that specifically bind to a lung tumor protein. As  
10 used herein, an antibody, or antigen-binding fragment thereof, is said to "specifically bind" to a lung tumor protein if it reacts at a detectable level (within, for example, an ELISA) with a lung tumor protein, and does not react detectably with unrelated proteins under similar conditions. As used herein, "binding" refers to a noncovalent association between two separate molecules such that a complex is formed. The ability to bind may  
15 be evaluated by, for example, determining a binding constant for the formation of the complex. The binding constant is the value obtained when the concentration of the complex is divided by the product of the component concentrations. In general, two compounds are said to "bind," in the context of the present invention, when the binding constant for complex formation exceeds about  $10^3$  L/mol. The binding constant may be  
20 determined using methods well known in the art.

Binding agents may be further capable of differentiating between patients with and without a cancer, such as lung cancer, using the representative assays provided herein. In other words, antibodies or other binding agents that bind to a lung tumor protein will generate a signal indicating the presence of a cancer in at least about  
25 20% of patients with the disease, and will generate a negative signal indicating the absence of the disease in at least about 90% of individuals without the cancer. To determine whether a binding agent satisfies this requirement, biological samples (*e.g.*, blood, sera, urine and/or tumor biopsies) from patients with and without a cancer (as determined using standard clinical tests) may be assayed as described herein for the  
30 presence of polypeptides that bind to the binding agent. It will be apparent that a statistically significant number of samples with and without the disease should be

assayed. Each binding agent should satisfy the above criteria; however, those of ordinary skill in the art will recognize that binding agents may be used in combination to improve sensitivity.

Any agent that satisfies the above requirements may be a binding agent.

5 For example, a binding agent may be a ribosome, with or without a peptide component, an RNA molecule or a polypeptide. In a preferred embodiment, a binding agent is an antibody or an antigen-binding fragment thereof. Antibodies may be prepared by any of a variety of techniques known to those of ordinary skill in the art. *See, e.g.,* Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In  
10 general, antibodies can be produced by cell culture techniques, including the generation of monoclonal antibodies as described herein, or via transfection of antibody genes into suitable bacterial or mammalian cell hosts, in order to allow for the production of recombinant antibodies. In one technique, an immunogen comprising the polypeptide is initially injected into any of a wide variety of mammals (*e.g.,* mice, rats, rabbits, sheep  
15 or goats). In this step, the polypeptides of this invention may serve as the immunogen without modification. Alternatively, particularly for relatively short polypeptides, a superior immune response may be elicited if the polypeptide is joined to a carrier protein, such as bovine serum albumin or keyhole limpet hemocyanin. The immunogen is injected into the animal host, preferably according to a predetermined schedule  
20 incorporating one or more booster immunizations, and the animals are bled periodically. Polyclonal antibodies specific for the polypeptide may then be purified from such antisera by, for example, affinity chromatography using the polypeptide coupled to a suitable solid support.

Monoclonal antibodies specific for an antigenic polypeptide of interest  
25 may be prepared, for example, using the technique of Kohler and Milstein, *Eur. J. Immunol.* 6:511-519, 1976, and improvements thereto. Briefly, these methods involve the preparation of immortal cell lines capable of producing antibodies having the desired specificity (*i.e.,* reactivity with the polypeptide of interest). Such cell lines may be produced, for example, from spleen cells obtained from an animal immunized as  
30 described above. The spleen cells are then immortalized by, for example, fusion with a myeloma cell fusion partner, preferably one that is syngeneic with the immunized

animal. A variety of fusion techniques may be employed. For example, the spleen cells and myeloma cells may be combined with a nonionic detergent for a few minutes and then plated at low density on a selective medium that supports the growth of hybrid cells, but not myeloma cells. A preferred selection technique uses HAT (hypoxanthine, aminopterin, thymidine) selection. After a sufficient time, usually about 1 to 2 weeks, colonies of hybrids are observed. Single colonies are selected and their culture supernatants tested for binding activity against the polypeptide. Hybridomas having high reactivity and specificity are preferred.

Monoclonal antibodies may be isolated from the supernatants of growing hybridoma colonies. In addition, various techniques may be employed to enhance the yield, such as injection of the hybridoma cell line into the peritoneal cavity of a suitable vertebrate host, such as a mouse. Monoclonal antibodies may then be harvested from the ascites fluid or the blood. Contaminants may be removed from the antibodies by conventional techniques, such as chromatography, gel filtration, precipitation, and extraction. The polypeptides of this invention may be used in the purification process in, for example, an affinity chromatography step.

Within certain embodiments, the use of antigen-binding fragments of antibodies may be preferred. Such fragments include Fab fragments, which may be prepared using standard techniques. Briefly, immunoglobulins may be purified from rabbit serum by affinity chromatography on Protein A bead columns (Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988) and digested by papain to yield Fab and Fc fragments. The Fab and Fc fragments may be separated by affinity chromatography on protein A bead columns.

Monoclonal antibodies of the present invention may be coupled to one or more therapeutic agents. Suitable agents in this regard include radionuclides, differentiation inducers, drugs, toxins, and derivatives thereof. Preferred radionuclides include  $^{90}\text{Y}$ ,  $^{123}\text{I}$ ,  $^{125}\text{I}$ ,  $^{131}\text{I}$ ,  $^{186}\text{Re}$ ,  $^{188}\text{Re}$ ,  $^{211}\text{At}$ , and  $^{212}\text{Bi}$ . Preferred drugs include methotrexate, and pyrimidine and purine analogs. Preferred differentiation inducers include phorbol esters and butyric acid. Preferred toxins include ricin, abrin, diphtheria toxin, cholera toxin, gelonin, *Pseudomonas* exotoxin, *Shigella* toxin, and pokeweed antiviral protein.

A therapeutic agent may be coupled (*e.g.*, covalently bonded) to a suitable monoclonal antibody either directly or indirectly (*e.g.*, via a linker group). A direct reaction between an agent and an antibody is possible when each possesses a substituent capable of reacting with the other. For example, a nucleophilic group, such as an amino or sulfhydryl group, on one may be capable of reacting with a carbonyl-containing group, such as an anhydride or an acid halide, or with an alkyl group containing a good leaving group (*e.g.*, a halide) on the other.

Alternatively, it may be desirable to couple a therapeutic agent and an antibody via a linker group. A linker group can function as a spacer to distance an antibody from an agent in order to avoid interference with binding capabilities. A linker group can also serve to increase the chemical reactivity of a substituent on an agent or an antibody, and thus increase the coupling efficiency. An increase in chemical reactivity may also facilitate the use of agents, or functional groups on agents, which otherwise would not be possible.

It will be evident to those skilled in the art that a variety of bifunctional or polyfunctional reagents, both homo- and hetero-functional (such as those described in the catalog of the Pierce Chemical Co., Rockford, IL), may be employed as the linker group. Coupling may be effected, for example, through amino groups, carboxyl groups, sulfhydryl groups or oxidized carbohydrate residues. There are numerous references describing such methodology, *e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.

Where a therapeutic agent is more potent when free from the antibody portion of the immunoconjugates of the present invention, it may be desirable to use a linker group which is cleavable during or upon internalization into a cell. A number of different cleavable linker groups have been described. The mechanisms for the intracellular release of an agent from these linker groups include cleavage by reduction of a disulfide bond (*e.g.*, U.S. Patent No. 4,489,710, to Spitler), by irradiation of a photolabile bond (*e.g.*, U.S. Patent No. 4,625,014, to Senter et al.), by hydrolysis of derivatized amino acid side chains (*e.g.*, U.S. Patent No. 4,638,045, to Kohn et al.), by serum complement-mediated hydrolysis (*e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.), and acid-catalyzed hydrolysis (*e.g.*, U.S. Patent No. 4,569,789, to Blattler et al.).

It may be desirable to couple more than one agent to an antibody. In one



embodiment, multiple molecules of an agent are coupled to one antibody molecule. In another embodiment, more than one type of agent may be coupled to one antibody. Regardless of the particular embodiment, immunoconjugates with more than one agent may be prepared in a variety of ways. For example, more than one agent may be coupled directly to an antibody molecule, or linkers which provide multiple sites for attachment can be used. Alternatively, a carrier can be used.

A carrier may bear the agents in a variety of ways, including covalent bonding either directly or via a linker group. Suitable carriers include proteins such as albumins (*e.g.*, U.S. Patent No. 4,507,234, to Kato et al.), peptides and polysaccharides such as aminodextran (*e.g.*, U.S. Patent No. 4,699,784, to Shih et al.). A carrier may also bear an agent by noncovalent bonding or by encapsulation, such as within a liposome vesicle (*e.g.*, U.S. Patent Nos. 4,429,008 and 4,873,088). Carriers specific for radionuclide agents include radiohalogenated small molecules and chelating compounds. For example, U.S. Patent No. 4,735,792 discloses representative radiohalogenated small molecules and their synthesis. A radionuclide chelate may be formed from chelating compounds that include those containing nitrogen and sulfur atoms as the donor atoms for binding the metal, or metal oxide, radionuclide. For example, U.S. Patent No. 4,673,562, to Davison et al. discloses representative chelating compounds and their synthesis.

A variety of routes of administration for the antibodies and immunoconjugates may be used. Typically, administration will be intravenous, intramuscular, subcutaneous or in the bed of a resected tumor. It will be evident that the precise dose of the antibody/immunoconjugate will vary depending upon the antibody used, the antigen density on the tumor, and the rate of clearance of the antibody.

### T CELLS

Immunotherapeutic compositions may also, or alternatively, comprise T cells specific for a lung tumor protein. Such cells may generally be prepared *in vitro* or *ex vivo*, using standard procedures. For example, T cells may be isolated from bone marrow, peripheral blood, or a fraction of bone marrow or peripheral blood of a patient, using a commercially available cell separation system, such as the ISOLEX™ system,



available from Nexell Therapeutics Inc., Irvine, CA (see also U.S. Patent No. 5,240,856; U.S. Patent No. 5,215,926; WO 89/06280; WO 91/16116 and WO 92/07243). Alternatively, T cells may be derived from related or unrelated humans, non-human mammals, cell lines or cultures.

5 T cells may be stimulated with a lung tumor polypeptide, polynucleotide encoding a lung tumor polypeptide and/or an antigen presenting cell (APC) that expresses such a polypeptide. Such stimulation is performed under conditions and for a time sufficient to permit the generation of T cells that are specific for the polypeptide. Preferably, a lung tumor polypeptide or polynucleotide is present within a delivery  
10 vehicle, such as a microsphere, to facilitate the generation of specific T cells.

T cells are considered to be specific for a lung tumor polypeptide if the T cells kill target cells coated with the polypeptide or expressing a gene encoding the polypeptide. T cell specificity may be evaluated using any of a variety of standard techniques. For example, within a chromium release assay or proliferation assay, a  
15 stimulation index of more than two fold increase in lysis and/or proliferation, compared to negative controls, indicates T cell specificity. Such assays may be performed, for example, as described in Chen et al., *Cancer Res.* 54:1065-1070, 1994. Alternatively, detection of the proliferation of T cells may be accomplished by a variety of known techniques. For example, T cell proliferation can be detected by measuring an increased  
20 rate of DNA synthesis (e.g., by pulse-labeling cultures of T cells with tritiated thymidine and measuring the amount of tritiated thymidine incorporated into DNA). Contact with a lung tumor polypeptide (100 ng/ml - 100 µg/ml, preferably 200 ng/ml - 25 µg/ml) for 3 - 7 days should result in at least a two fold increase in proliferation of the T cells. Contact as described above for 2-3 hours should result in activation of the T  
25 cells, as measured using standard cytokine assays in which a two fold increase in the level of cytokine release (e.g., TNF or IFN-γ) is indicative of T cell activation (see Coligan et al., *Current Protocols in Immunology*, vol. 1, Wiley Interscience (Greene 1998)). T cells that have been activated in response to a lung tumor polypeptide, polynucleotide or polypeptide-expressing APC may be CD4<sup>+</sup> and/or CD8<sup>+</sup>. Lung tumor  
30 protein-specific T cells may be expanded using standard techniques. Within preferred embodiments, the T cells are derived from either a patient or a related, or unrelated,

donor and are administered to the patient following stimulation and expansion.

For therapeutic purposes, CD4<sup>+</sup> or CD8<sup>+</sup> T cells that proliferate in response to a lung tumor polypeptide, polynucleotide or APC can be expanded in number either *in vitro* or *in vivo*. Proliferation of such T cells *in vitro* may be accomplished in a variety of ways. For example, the T cells can be re-exposed to a lung tumor polypeptide, or a short peptide corresponding to an immunogenic portion of such a polypeptide, with or without the addition of T cell growth factors, such as interleukin-2, and/or stimulator cells that synthesize a lung tumor polypeptide. Alternatively, one or more T cells that proliferate in the presence of a lung tumor protein can be expanded in number by cloning. Methods for cloning cells are well known in the art, and include limiting dilution.

#### PHARMACEUTICAL COMPOSITIONS AND VACCINES

Within certain aspects, polypeptides, polynucleotides, T cells and/or binding agents disclosed herein may be incorporated into pharmaceutical compositions or immunogenic compositions (*i.e.*, vaccines). Pharmaceutical compositions comprise one or more such compounds and a physiologically acceptable carrier. Vaccines may comprise one or more such compounds and an immunostimulant. An immunostimulant may be any substance that enhances or potentiates an immune response to an exogenous antigen. Examples of immunostimulants include adjuvants, biodegradable microspheres (*e.g.*, polylactic galactide) and liposomes (into which the compound is incorporated; *see e.g.*, Fullerton, U.S. Patent No. 4,235,877). Vaccine preparation is generally described in, for example, M.F. Powell and M.J. Newman, eds., "Vaccine Design (the subunit and adjuvant approach)," Plenum Press (NY, 1995). Pharmaceutical compositions and vaccines within the scope of the present invention may also contain other compounds, which may be biologically active or inactive. For example, one or more immunogenic portions of other tumor antigens may be present, either incorporated into a fusion polypeptide or as a separate compound, within the composition or vaccine.

A pharmaceutical composition or vaccine may contain DNA encoding one or more of the polypeptides as described above, such that the polypeptide is

generated *in situ*. As noted above, the DNA may be present within any of a variety of delivery systems known to those of ordinary skill in the art, including nucleic acid expression systems, bacteria and viral expression systems. Numerous gene delivery techniques are well known in the art, such as those described by Rolland, *Crit. Rev. Therap. Drug Carrier Systems* 15:143-198, 1998, and references cited therein. Appropriate nucleic acid expression systems contain the necessary DNA sequences for expression in the patient (such as a suitable promoter and terminating signal). Bacterial delivery systems involve the administration of a bacterium (such as *Bacillus-Calmette-Guerrin*) that expresses an immunogenic portion of the polypeptide on its cell surface or secretes such an epitope. In a preferred embodiment, the DNA may be introduced using a viral expression system (*e.g.*, vaccinia or other pox virus, retrovirus, or adenovirus), which may involve the use of a non-pathogenic (defective), replication competent virus. Suitable systems are disclosed, for example, in Fisher-Hoch et al., *Proc. Natl. Acad. Sci. USA* 86:317-321, 1989; Flexner et al., *Ann. N.Y. Acad. Sci.* 569:86-103, 1989; Flexner et al., *Vaccine* 8:17-21, 1990; U.S. Patent Nos. 4,603,112, 4,769,330, and 5,017,487; WO 89/01973; U.S. Patent No. 4,777,127; GB 2,200,651; EP 0,345,242; WO 91/02805; Berkner, *Biotechniques* 6:616-627, 1988; Rosenfeld et al., *Science* 252:431-434, 1991; Kolls et al., *Proc. Natl. Acad. Sci. USA* 91:215-219, 1994; Kass-Eisler et al., *Proc. Natl. Acad. Sci. USA* 90:11498-11502, 1993; Guzman et al., *Circulation* 88:2838-2848, 1993; and Guzman et al., *Cir. Res.* 73:1202-1207, 1993. Techniques for incorporating DNA into such expression systems are well known to those of ordinary skill in the art. The DNA may also be "naked," as described, for example, in Ulmer et al., *Science* 259:1745-1749, 1993 and reviewed by Cohen, *Science* 259:1691-1692, 1993. The uptake of naked DNA may be increased by coating the DNA onto biodegradable beads, which are efficiently transported into the cells.

While any suitable carrier known to those of ordinary skill in the art may be employed in the pharmaceutical compositions of this invention, the type of carrier will vary depending on the mode of administration. Compositions of the present invention may be formulated for any appropriate manner of administration, including for example, topical, oral, nasal, intravenous, intracranial, intraperitoneal, subcutaneous or intramuscular administration. For parenteral administration, such as subcutaneous

injection, the carrier preferably comprises water, saline, alcohol, a fat, a wax or a buffer. For oral administration, any of the above carriers or a solid carrier, such as mannitol, lactose, starch, magnesium stearate, sodium saccharine, talcum, cellulose, glucose, sucrose, and magnesium carbonate, may be employed. Biodegradable microspheres  
5 (e.g., polylactate polyglycolate) may also be employed as carriers for the pharmaceutical compositions of this invention. Suitable biodegradable microspheres are disclosed, for example, in U.S. Patent Nos. 4,897,268 and 5,075,109.

Such compositions may also comprise buffers (e.g., neutral buffered saline or phosphate buffered saline), carbohydrates (e.g., glucose, mannose, sucrose or  
10 dextrans), mannitol, proteins, polypeptides or amino acids such as glycine, antioxidants, chelating agents such as EDTA or glutathione, adjuvants (e.g., aluminum hydroxide) and/or preservatives. Alternatively, compositions of the present invention may be formulated as a lyophilizate. Compounds may also be encapsulated within liposomes using well known technology.

15 Any of a variety of immunostimulants may be employed in the vaccines of this invention. For example, an adjuvant may be included. Most adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, *Bordetella pertussis* or *Mycobacterium tuberculosis* derived proteins. Suitable  
20 adjuvants are commercially available as, for example, Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized  
25 polysaccharides; polyphosphazenes; biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF or interleukin-2, -7, or -12, may also be used as adjuvants.

Within the vaccines provided herein, the adjuvant composition is preferably designed to induce an immune response predominantly of the Th1 type.  
30 High levels of Th1-type cytokines (e.g., IFN- $\gamma$ , TNF $\alpha$ , IL-2 and IL-12) tend to favor the induction of cell mediated immune responses to an administered antigen. In contrast,

high levels of Th2-type cytokines (e.g., IL-4, IL-5, IL-6 and IL-10) tend to favor the induction of humoral immune responses. Following application of a vaccine as provided herein, a patient will support an immune response that includes Th1- and Th2-type responses. Within a preferred embodiment, in which a response is predominantly Th1-type, the level of Th1-type cytokines will increase to a greater extent than the level of Th2-type cytokines. The levels of these cytokines may be readily assessed using standard assays. For a review of the families of cytokines, see Mosmann and Coffman, *Ann. Rev. Immunol.* 7:145-173, 1989.

Preferred adjuvants for use in eliciting a predominantly Th1-type response include, for example, a combination of monophosphoryl lipid A, preferably 3-de-O-acylated monophosphoryl lipid A (3D-MPL), together with an aluminum salt. MPL adjuvants are available from Ribi ImmunoChem Research Inc. (Hamilton, MT) (see US Patent Nos. 4,436,727; 4,877,611; 4,866,034 and 4,912,094). CpG-containing oligonucleotides (in which the CpG dinucleotide is unmethylated) also induce a predominantly Th1 response. Such oligonucleotides are well known and are described, for example, in WO 96/02555. Another preferred adjuvant is a saponin, preferably QS21, which may be used alone or in combination with other adjuvants. For example, an enhanced system involves the combination of a monophosphoryl lipid A and saponin derivative, such as the combination of QS21 and 3D-MPL as described in WO 94/00153, or a less reactogenic composition where the QS21 is quenched with cholesterol, as described in WO 96/33739. Other preferred formulations comprises an oil-in-water emulsion and tocopherol. A particularly potent adjuvant formulation involving QS21, 3D-MPL and tocopherol in an oil-in-water emulsion is described in WO 95/17210. Any vaccine provided herein may be prepared using well known methods that result in a combination of antigen, immune response enhancer and a suitable carrier or excipient.

The compositions described herein may be administered as part of a sustained release formulation (i.e., a formulation such as a capsule, sponge or gel (composed of polysaccharides, for example) that effects a slow release of compound following administration). Such formulations may generally be prepared using well known technology and administered by, for example, oral, rectal or subcutaneous



implantation, or by implantation at the desired target site. Sustained-release formulations may contain a polypeptide, polynucleotide or antibody dispersed in a carrier matrix and/or contained within a reservoir surrounded by a rate controlling membrane. Carriers for use within such formulations are biocompatible, and may also  
5 be biodegradable; preferably the formulation provides a relatively constant level of active component release. The amount of active compound contained within a sustained release formulation depends upon the site of implantation, the rate and expected duration of release and the nature of the condition to be treated or prevented.

Any of a variety of delivery vehicles may be employed within  
10 pharmaceutical compositions and vaccines to facilitate production of an antigen-specific immune response that targets tumor cells. Delivery vehicles include antigen presenting cells (APCs), such as dendritic cells, macrophages, B cells, monocytes and other cells that may be engineered to be efficient APCs. Such cells may, but need not, be genetically modified to increase the capacity for presenting the antigen, to improve  
15 activation and/or maintenance of the T cell response, to have anti-tumor effects *per se* and/or to be immunologically compatible with the receiver (*i.e.*, matched HLA haplotype). APCs may generally be isolated from any of a variety of biological fluids and organs, including tumor and peritumoral tissues, and may be autologous, allogeneic, syngeneic or xenogeneic cells.

20 Certain preferred embodiments of the present invention use dendritic cells or progenitors thereof as antigen-presenting cells. Dendritic cells are highly potent APCs (Banchereau and Steinman, *Nature* 392:245-251, 1998) and have been shown to be effective as a physiological adjuvant for eliciting prophylactic or therapeutic antitumor immunity (*see* Timmerman and Levy, *Ann. Rev. Med.* 50:507-529, 1999). In  
25 general, dendritic cells may be identified based on their typical shape (stellate *in situ*, with marked cytoplasmic processes (dendrites) visible *in vitro*), their ability to take up, process and present antigens with high efficiency, and their ability to activate naïve T cell responses. Dendritic cells may, of course, be engineered to express specific cell-surface receptors or ligands that are not commonly found on dendritic cells *in vivo* or *ex*  
30 *vivo*, and such modified dendritic cells are contemplated by the present invention. As an alternative to dendritic cells, secreted vesicles antigen-loaded dendritic cells (called



exosomes) may be used within a vaccine (see Zitvogel et al., *Nature Med.* 4:594-600, 1998).

Dendritic cells and progenitors may be obtained from peripheral blood, bone marrow, tumor-infiltrating cells, peritumoral tissues-infiltrating cells, lymph nodes, spleen, skin, umbilical cord blood or any other suitable tissue or fluid. For example, dendritic cells may be differentiated *ex vivo* by adding a combination of cytokines such as GM-CSF, IL-4, IL-13 and/or TNF $\alpha$  to cultures of monocytes harvested from peripheral blood. Alternatively, CD34 positive cells harvested from peripheral blood, umbilical cord blood or bone marrow may be differentiated into dendritic cells by adding to the culture medium combinations of GM-CSF, IL-3, TNF $\alpha$ , CD40 ligand, LPS, flt3 ligand and/or other compound(s) that induce maturation and proliferation of dendritic cells.

Dendritic cells are conveniently categorized as "immature" and "mature" cells, which allows a simple way to discriminate between two well characterized phenotypes. However, this nomenclature should not be construed to exclude all possible intermediate stages of differentiation. Immature dendritic cells are characterized as APC with a high capacity for antigen uptake and processing, which correlates with the high expression of Fc $\gamma$  receptor, mannose receptor and DEC-205 marker. The mature phenotype is typically characterized by a lower expression of these markers, but a high expression of cell surface molecules responsible for T cell activation such as class I and class II MHC, adhesion molecules (*e.g.*, CD54 and CD11) and costimulatory molecules (*e.g.*, CD40, CD80, CD86 and 4-1BB).

APCs may generally be transfected with a polynucleotide encoding a lung tumor protein (or portion or other variant thereof) such that the lung tumor polypeptide, or an immunogenic portion thereof, is expressed on the cell surface. Such transfection may take place *ex vivo*, and a composition or vaccine comprising such transfected cells may then be used for therapeutic purposes, as described herein. Alternatively, a gene delivery vehicle that targets a dendritic or other antigen presenting cell may be administered to a patient, resulting in transfection that occurs *in vivo*. *In vivo* and *ex vivo* transfection of dendritic cells, for example, may generally be performed using any methods known in the art, such as those described in WO

97/24447, or the gene gun approach described by Mahvi et al., *Immunology and cell Biology* 75:456-460, 1997. Antigen loading of dendritic cells may be achieved by incubating dendritic cells or progenitor cells with the lung tumor polypeptide, DNA (naked or within a plasmid vector) or RNA; or with antigen-expressing recombinant  
5 bacterium or viruses (e.g., vaccinia, fowlpox, adenovirus or lentivirus vectors). Prior to loading, the polypeptide may be covalently conjugated to an immunological partner that provides T cell help (e.g., a carrier molecule). Alternatively, a dendritic cell may be pulsed with a non-conjugated immunological partner, separately or in the presence of the polypeptide.

10

#### CANCER THERAPY

In further aspects of the present invention, the compositions described herein may be used for immunotherapy of cancer, such as lung cancer. Within such methods, pharmaceutical compositions and vaccines are typically administered to a  
15 patient. As used herein, a "patient" refers to any warm-blooded animal, preferably a human. A patient may or may not be afflicted with cancer. Accordingly, the above pharmaceutical compositions and vaccines may be used to prevent the development of a cancer or to treat a patient afflicted with a cancer. A cancer may be diagnosed using criteria generally accepted in the art, including the presence of a malignant tumor.  
20 Pharmaceutical compositions and vaccines may be administered either prior to or following surgical removal of primary tumors and/or treatment such as administration of radiotherapy or conventional chemotherapeutic drugs.

Within certain embodiments, immunotherapy may be active immunotherapy, in which treatment relies on the *in vivo* stimulation of the endogenous  
25 host immune system to react against tumors with the administration of immune response-modifying agents (such as polypeptides and polynucleotides disclosed herein).

Within other embodiments, immunotherapy may be passive immunotherapy, in which treatment involves the delivery of agents with established tumor-immune reactivity (such as effector cells or antibodies) that can directly or  
30 indirectly mediate antitumor effects and does not necessarily depend on an intact host immune system. Examples of effector cells include T cells as discussed above, T

lymphocytes (such as CD8<sup>+</sup> cytotoxic T lymphocytes and CD4<sup>+</sup> T-helper tumor-infiltrating lymphocytes), killer cells (such as Natural Killer cells and lymphokine-activated killer cells), B cells and antigen-presenting cells (such as dendritic cells and macrophages) expressing a polypeptide provided herein. T cell receptors and antibody  
5 receptors specific for the polypeptides recited herein may be cloned, expressed and transferred into other vectors or effector cells for adoptive immunotherapy. The polypeptides provided herein may also be used to generate antibodies or anti-idiotypic antibodies (as described above and in U.S. Patent No. 4,918,164) for passive immunotherapy.

10 Effector cells may generally be obtained in sufficient quantities for adoptive immunotherapy by growth *in vitro*, as described herein. Culture conditions for expanding single antigen-specific effector cells to several billion in number with retention of antigen recognition *in vivo* are well known in the art. Such *in vitro* culture conditions typically use intermittent stimulation with antigen, often in the presence of  
15 cytokines (such as IL-2) and non-dividing feeder cells. As noted above, immunoreactive polypeptides as provided herein may be used to rapidly expand antigen-specific T cell cultures in order to generate a sufficient number of cells for immunotherapy. In particular, antigen-presenting cells, such as dendritic, macrophage, monocyte, fibroblast or B cells, may be pulsed with immunoreactive polypeptides or  
20 transfected with one or more polynucleotides using standard techniques well known in the art. For example, antigen-presenting cells can be transfected with a polynucleotide having a promoter appropriate for increasing expression in a recombinant virus or other expression system. Cultured effector cells for use in therapy must be able to grow and distribute widely, and to survive long term *in vivo*. Studies have shown that cultured  
25 effector cells can be induced to grow *in vivo* and to survive long term in substantial numbers by repeated stimulation with antigen supplemented with IL-2 (see, for example, Cheever et al., *Immunological Reviews* 157:177, 1997).

Alternatively, a vector expressing a polypeptide recited herein may be introduced into antigen presenting cells taken from a patient and clonally propagated *ex*  
30 *vivo* for transplant back into the same patient. Transfected cells may be reintroduced into the patient using any means known in the art, preferably in sterile form by

intravenous, intracavitary, intraperitoneal or intratumor administration.

Routes and frequency of administration of the therapeutic compositions disclosed herein, as well as dosage, will vary from individual to individual, and may be readily established using standard techniques. In general, the pharmaceutical compositions and vaccines may be administered by injection (*e.g.*, intracutaneous, intramuscular, intravenous or subcutaneous), intranasally (*e.g.*, by aspiration) or orally. Preferably, between 1 and 10 doses may be administered over a 52 week period. Preferably, 6 doses are administered, at intervals of 1 month, and booster vaccinations may be given periodically thereafter. Alternate protocols may be appropriate for individual patients. A suitable dose is an amount of a compound that, when administered as described above, is capable of promoting an anti-tumor immune response, and is at least 10-50% above the basal (*i.e.*, untreated) level. Such response can be monitored by measuring the anti-tumor antibodies in a patient or by vaccine-dependent generation of cytolytic effector cells capable of killing the patient's tumor cells *in vitro*. Such vaccines should also be capable of causing an immune response that leads to an improved clinical outcome (*e.g.*, more frequent remissions, complete or partial or longer disease-free survival) in vaccinated patients as compared to non-vaccinated patients. In general, for pharmaceutical compositions and vaccines comprising one or more polypeptides, the amount of each polypeptide present in a dose ranges from about 25  $\mu$ g to 5 mg per kg of host. Suitable dose sizes will vary with the size of the patient, but will typically range from about 0.1 mL to about 5 mL.

In general, an appropriate dosage and treatment regimen provides the active compound(s) in an amount sufficient to provide therapeutic and/or prophylactic benefit. Such a response can be monitored by establishing an improved clinical outcome (*e.g.*, more frequent remissions, complete or partial, or longer disease-free survival) in treated patients as compared to non-treated patients. Increases in preexisting immune responses to a lung tumor protein generally correlate with an improved clinical outcome. Such immune responses may generally be evaluated using standard proliferation, cytotoxicity or cytokine assays, which may be performed using samples obtained from a patient before and after treatment.

### METHODS FOR DETECTING CANCER

In general, a cancer may be detected in a patient based on the presence of one or more lung tumor proteins and/or polynucleotides encoding such proteins in a biological sample (for example, blood, sera, urine and/or tumor biopsies) obtained from the patient. In other words, such proteins may be used as markers to indicate the presence or absence of a cancer such as lung cancer. In addition, such proteins may be useful for the detection of other cancers. The binding agents provided herein generally permit detection of the level of antigen that binds to the agent in the biological sample. Polynucleotide primers and probes may be used to detect the level of mRNA encoding a tumor protein, which is also indicative of the presence or absence of a cancer. In general, a lung tumor sequence should be present at a level that is at least three fold higher in tumor tissue than in normal tissue

There are a variety of assay formats known to those of ordinary skill in the art for using a binding agent to detect polypeptide markers in a sample. See, e.g., Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In general, the presence or absence of a cancer in a patient may be determined by (a) contacting a biological sample obtained from a patient with a binding agent; (b) detecting in the sample a level of polypeptide that binds to the binding agent; and (c) comparing the level of polypeptide with a predetermined cut-off value.

In a preferred embodiment, the assay involves the use of binding agent immobilized on a solid support to bind to and remove the polypeptide from the remainder of the sample. The bound polypeptide may then be detected using a detection reagent that contains a reporter group and specifically binds to the binding agent/polypeptide complex. Such detection reagents may comprise, for example, a binding agent that specifically binds to the polypeptide or an antibody or other agent that specifically binds to the binding agent, such as an anti-immunoglobulin, protein G, protein A or a lectin. Alternatively, a competitive assay may be utilized, in which a polypeptide is labeled with a reporter group and allowed to bind to the immobilized binding agent after incubation of the binding agent with the sample. The extent to which components of the sample inhibit the binding of the labeled polypeptide to the binding agent is indicative of the reactivity of the sample with the immobilized binding



agent. Suitable polypeptides for use within such assays include full length lung tumor proteins and portions thereof to which the binding agent binds, as described above.

The solid support may be any material known to those of ordinary skill in the art to which the tumor protein may be attached. For example, the solid support  
5 may be a test well in a microtiter plate or a nitrocellulose or other suitable membrane. Alternatively, the support may be a bead or disc, such as glass, fiberglass, latex or a plastic material such as polystyrene or polyvinylchloride. The support may also be a magnetic particle or a fiber optic sensor, such as those disclosed, for example, in U.S. Patent No. 5,359,681. The binding agent may be immobilized on the solid support  
10 using a variety of techniques known to those of skill in the art, which are amply described in the patent and scientific literature. In the context of the present invention, the term "immobilization" refers to both noncovalent association, such as adsorption, and covalent attachment (which may be a direct linkage between the agent and functional groups on the support or may be a linkage by way of a cross-linking agent).  
15 Immobilization by adsorption to a well in a microtiter plate or to a membrane is preferred. In such cases, adsorption may be achieved by contacting the binding agent, in a suitable buffer, with the solid support for a suitable amount of time. The contact time varies with temperature, but is typically between about 1 hour and about 1 day. In general, contacting a well of a plastic microtiter plate (such as polystyrene or  
20 polyvinylchloride) with an amount of binding agent ranging from about 10 ng to about 10  $\mu$ g, and preferably about 100 ng to about 1  $\mu$ g, is sufficient to immobilize an adequate amount of binding agent.

Covalent attachment of binding agent to a solid support may generally be achieved by first reacting the support with a bifunctional reagent that will react with  
25 both the support and a functional group, such as a hydroxyl or amino group, on the binding agent. For example, the binding agent may be covalently attached to supports having an appropriate polymer coating using benzoquinone or by condensation of an aldehyde group on the support with an amine and an active hydrogen on the binding partner (*see, e.g.,* Pierce Immunotechnology Catalog and Handbook, 1991, at  
30 A12-A13).

In certain embodiments, the assay is a two-antibody sandwich assay.



This assay may be performed by first contacting an antibody that has been immobilized on a solid support, commonly the well of a microtiter plate, with the sample, such that polypeptides within the sample are allowed to bind to the immobilized antibody. Unbound sample is then removed from the immobilized polypeptide-antibody complexes and a detection reagent (preferably a second antibody capable of binding to a different site on the polypeptide) containing a reporter group is added. The amount of detection reagent that remains bound to the solid support is then determined using a method appropriate for the specific reporter group.

More specifically, once the antibody is immobilized on the support as described above, the remaining protein binding sites on the support are typically blocked. Any suitable blocking agent known to those of ordinary skill in the art, such as bovine serum albumin or Tween 20™ (Sigma Chemical Co., St. Louis, MO). The immobilized antibody is then incubated with the sample, and polypeptide is allowed to bind to the antibody. The sample may be diluted with a suitable diluent, such as phosphate-buffered saline (PBS) prior to incubation. In general, an appropriate contact time (*i.e.*, incubation time) is a period of time that is sufficient to detect the presence of polypeptide within a sample obtained from an individual with lung cancer. Preferably, the contact time is sufficient to achieve a level of binding that is at least about 95% of that achieved at equilibrium between bound and unbound polypeptide. Those of ordinary skill in the art will recognize that the time necessary to achieve equilibrium may be readily determined by assaying the level of binding that occurs over a period of time. At room temperature, an incubation time of about 30 minutes is generally sufficient.

Unbound sample may then be removed by washing the solid support with an appropriate buffer, such as PBS containing 0.1% Tween 20™. The second antibody, which contains a reporter group, may then be added to the solid support. Preferred reporter groups include those groups recited above.

The detection reagent is then incubated with the immobilized antibody-polypeptide complex for an amount of time sufficient to detect the bound polypeptide. An appropriate amount of time may generally be determined by assaying the level of binding that occurs over a period of time. Unbound detection reagent is then removed

and bound detection reagent is detected using the reporter group. The method employed for detecting the reporter group depends upon the nature of the reporter group. For radioactive groups, scintillation counting or autoradiographic methods are generally appropriate. Spectroscopic methods may be used to detect dyes, luminescent groups and fluorescent groups. Biotin may be detected using avidin, coupled to a different reporter group (commonly a radioactive or fluorescent group or an enzyme). Enzyme reporter groups may generally be detected by the addition of substrate (generally for a specific period of time), followed by spectroscopic or other analysis of the reaction products.

To determine the presence or absence of a cancer, such as lung cancer, the signal detected from the reporter group that remains bound to the solid support is generally compared to a signal that corresponds to a predetermined cut-off value. In one preferred embodiment, the cut-off value for the detection of a cancer is the average mean signal obtained when the immobilized antibody is incubated with samples from patients without the cancer. In general, a sample generating a signal that is three standard deviations above the predetermined cut-off value is considered positive for the cancer. In an alternate preferred embodiment, the cut-off value is determined using a Receiver Operator Curve, according to the method of Sackett et al., *Clinical Epidemiology: A Basic Science for Clinical Medicine*, Little Brown and Co., 1985, p. 106-7. Briefly, in this embodiment, the cut-off value may be determined from a plot of pairs of true positive rates (*i.e.*, sensitivity) and false positive rates (100%-specificity) that correspond to each possible cut-off value for the diagnostic test result. The cut-off value on the plot that is the closest to the upper left-hand corner (*i.e.*, the value that encloses the largest area) is the most accurate cut-off value, and a sample generating a signal that is higher than the cut-off value determined by this method may be considered positive. Alternatively, the cut-off value may be shifted to the left along the plot, to minimize the false positive rate, or to the right, to minimize the false negative rate. In general, a sample generating a signal that is higher than the cut-off value determined by this method is considered positive for a cancer.

In a related embodiment, the assay is performed in a flow-through or strip test format, wherein the binding agent is immobilized on a membrane, such as

nitrocellulose. In the flow-through test, polypeptides within the sample bind to the immobilized binding agent as the sample passes through the membrane. A second, labeled binding agent then binds to the binding agent-polypeptide complex as a solution containing the second binding agent flows through the membrane. The detection of bound second binding agent may then be performed as described above. In the strip test format, one end of the membrane to which binding agent is bound is immersed in a solution containing the sample. The sample migrates along the membrane through a region containing second binding agent and to the area of immobilized binding agent. Concentration of second binding agent at the area of immobilized antibody indicates the presence of a cancer. Typically, the concentration of second binding agent at that site generates a pattern, such as a line, that can be read visually. The absence of such a pattern indicates a negative result. In general, the amount of binding agent immobilized on the membrane is selected to generate a visually discernible pattern when the biological sample contains a level of polypeptide that would be sufficient to generate a positive signal in the two-antibody sandwich assay, in the format discussed above. Preferred binding agents for use in such assays are antibodies and antigen-binding fragments thereof. Preferably, the amount of antibody immobilized on the membrane ranges from about 25 ng to about 1  $\mu$ g, and more preferably from about 50 ng to about 500 ng. Such tests can typically be performed with a very small amount of biological sample.

Of course, numerous other assay protocols exist that are suitable for use with the tumor proteins or binding agents of the present invention. The above descriptions are intended to be exemplary only. For example, it will be apparent to those of ordinary skill in the art that the above protocols may be readily modified to use lung tumor polypeptides to detect antibodies that bind to such polypeptides in a biological sample. The detection of such lung tumor protein specific antibodies may correlate with the presence of a cancer.

A cancer may also, or alternatively, be detected based on the presence of T cells that specifically react with a lung tumor protein in a biological sample. Within certain methods, a biological sample comprising CD4<sup>+</sup> and/or CD8<sup>+</sup> T cells isolated from a patient is incubated with a lung tumor polypeptide, a polynucleotide encoding

such a polypeptide and/or an APC that expresses at least an immunogenic portion of such a polypeptide, and the presence or absence of specific activation of the T cells is detected. Suitable biological samples include, but are not limited to, isolated T cells. For example, T cells may be isolated from a patient by routine techniques (such as by  
5 Ficoll/Hypaque density gradient centrifugation of peripheral blood lymphocytes). T cells may be incubated *in vitro* for 2-9 days (typically 4 days) at 37°C with polypeptide (e.g., 5 - 25 µg/ml). It may be desirable to incubate another aliquot of a T cell sample in the absence of lung tumor polypeptide to serve as a control. For CD4<sup>+</sup> T cells, activation is preferably detected by evaluating proliferation of the T cells. For CD8<sup>+</sup> T  
10 cells, activation is preferably detected by evaluating cytolytic activity. A level of proliferation that is at least two fold greater and/or a level of cytolytic activity that is at least 20% greater than in disease-free patients indicates the presence of a cancer in the patient.

As noted above, a cancer may also, or alternatively, be detected based on  
15 the level of mRNA encoding a lung tumor protein in a biological sample. For example, at least two oligonucleotide primers may be employed in a polymerase chain reaction (PCR) based assay to amplify a portion of a lung tumor cDNA derived from a biological sample, wherein at least one of the oligonucleotide primers is specific for (*i.e.*, hybridizes to) a polynucleotide encoding the lung tumor protein. The amplified  
20 cDNA is then separated and detected using techniques well known in the art, such as gel electrophoresis. Similarly, oligonucleotide probes that specifically hybridize to a polynucleotide encoding a lung tumor protein may be used in a hybridization assay to detect the presence of polynucleotide encoding the tumor protein in a biological sample.

To permit hybridization under assay conditions, oligonucleotide primers  
25 and probes should comprise an oligonucleotide sequence that has at least about 60%, preferably at least about 75% and more preferably at least about 90%, identity to a portion of a polynucleotide encoding a lung tumor protein that is at least 10 nucleotides, and preferably at least 20 nucleotides, in length. Preferably, oligonucleotide primers and/or probes will hybridize to a polynucleotide encoding a polypeptide disclosed  
30 herein under moderately stringent conditions, as defined above. Oligonucleotide primers and/or probes which may be usefully employed in the diagnostic methods

described herein preferably are at least 10-40 nucleotides in length. In a preferred embodiment, the oligonucleotide primers comprise at least 10 contiguous nucleotides, more preferably at least 15 contiguous nucleotides, of a DNA molecule having a sequence recited in SEQ ID NOS: 1-31, 49-55, 63,64, 66, 68-72, 78-80, 84-92 and 217-389. Techniques for both PCR based assays and hybridization assays are well known in the art (*see*, for example, Mullis et al., *Cold Spring Harbor Symp. Quant. Biol.*, 51:263, 1987; Erlich ed., *PCR Technology*, Stockton Press, NY, 1989).

One preferred assay employs RT-PCR, in which PCR is applied in conjunction with reverse transcription. Typically, RNA is extracted from a biological sample, such as biopsy tissue, and is reverse transcribed to produce cDNA molecules. PCR amplification using at least one specific primer generates a cDNA molecule, which may be separated and visualized using, for example, gel electrophoresis. Amplification may be performed on biological samples taken from a test patient and from an individual who is not afflicted with a cancer. The amplification reaction may be performed on several dilutions of cDNA spanning two orders of magnitude. A two-fold or greater increase in expression in several dilutions of the test patient sample as compared to the same dilutions of the non-cancerous sample is typically considered positive.

In another embodiment, the disclosed compositions may be used as markers for the progression of cancer. In this embodiment, assays as described above for the diagnosis of a cancer may be performed over time, and the change in the level of reactive polypeptide(s) or polynucleotide evaluated. For example, the assays may be performed every 24-72 hours for a period of 6 months to 1 year, and thereafter performed as needed. In general, a cancer is progressing in those patients in whom the level of polypeptide or polynucleotide detected increases over time. In contrast, the cancer is not progressing when the level of reactive polypeptide or polynucleotide either remains constant or decreases with time.

Certain *in vivo* diagnostic assays may be performed directly on a tumor. One such assay involves contacting tumor cells with a binding agent. The bound binding agent may then be detected directly or indirectly via a reporter group. Such binding agents may also be used in histological applications. Alternatively,

polynucleotide probes may be used within such applications.

As noted above, to improve sensitivity, multiple lung tumor protein markers may be assayed within a given sample. It will be apparent that binding agents specific for different proteins provided herein may be combined within a single assay.

5 Further, multiple primers or probes may be used concurrently. The selection of tumor protein markers may be based on routine experiments to determine combinations that results in optimal sensitivity. In addition, or alternatively, assays for tumor proteins provided herein may be combined with assays for other known tumor antigens.

#### 10 DIAGNOSTIC KITS

The present invention further provides kits for use within any of the above diagnostic methods. Such kits typically comprise two or more components necessary for performing a diagnostic assay. Components may be compounds, reagents, containers and/or equipment. For example, one container within a kit may  
15 contain a monoclonal antibody or fragment thereof that specifically binds to a lung tumor protein. Such antibodies or fragments may be provided attached to a support material, as described above. One or more additional containers may enclose elements, such as reagents or buffers, to be used in the assay. Such kits may also, or alternatively, contain a detection reagent as described above that contains a reporter group suitable for  
20 direct or indirect detection of antibody binding.

Alternatively, a kit may be designed to detect the level of mRNA encoding a lung tumor protein in a biological sample. Such kits generally comprise at least one oligonucleotide probe or primer, as described above, that hybridizes to a polynucleotide encoding a lung tumor protein. Such an oligonucleotide may be used,  
25 for example, within a PCR or hybridization assay. Additional components that may be present within such kits include a second oligonucleotide and/or a diagnostic reagent or container to facilitate the detection of a polynucleotide encoding a lung tumor protein.

The following Examples are offered by way of illustration and not by way of limitation.



EXAMPLES

## Example 1

PREPARATION OF LUNG TUMOR-SPECIFIC cDNA SEQUENCES USING  
DIFFERENTIAL DISPLAY RT-PCR

This example illustrates the preparation of cDNA molecules encoding lung tumor-specific polypeptides using a differential display screen.

Tissue samples were prepared from lung tumor and normal tissue of a patient with lung cancer that was confirmed by pathology after removal of samples from the patient. Normal RNA and tumor RNA was extracted from the samples and mRNA was isolated and converted into cDNA using a (dT)<sub>12</sub>AG (SEQ ID NO: 47) anchored 3' primer. Differential display PCR was then executed using a randomly chosen primer (SEQ ID NO: 48). Amplification conditions were standard buffer containing 1.5 mM MgCl<sub>2</sub>, 20 pmol of primer, 500 pmol dNTP and 1 unit of Taq DNA polymerase (Perkin-Elmer, Branchburg, NJ). Forty cycles of amplification were performed using 94 °C denaturation for 30 seconds, 42 °C annealing for 1 minute and 72 °C extension for 30 seconds. Bands that were repeatedly observed to be specific to the RNA fingerprint pattern of the tumor were cut out of a silver stained gel, subcloned into the pGEM-T vector (Promega, Madison, WI) and sequenced. The isolated 3' sequences are provided in SEQ ID NO: 1-16.

Comparison of these sequences to those in the public databases using the BLASTN program, revealed no significant homologies to the sequences provided in SEQ ID NO: 1-11. To the best of the inventors' knowledge, none of the isolated DNA sequences have previously been shown to be expressed at a greater level in human lung tumor tissue than in normal lung tissue.

## Example 2

USE OF PATIENT SERA TO IDENTIFY DNA SEQUENCES ENCODING LUNG  
TUMOR ANTIGENS

5

This example illustrates the isolation of cDNA sequences encoding lung tumor antigens by expression screening of lung tumor samples with autologous patient sera.

10 A human lung tumor directional cDNA expression library was constructed employing the Lambda ZAP Express expression system (Stratagene, La Jolla, CA). Total RNA for the library was taken from a late SCID mouse passaged human squamous epithelial lung carcinoma and poly A+ RNA was isolated using the Message Maker kit (Gibco BRL, Gaithersburg, MD). The resulting library was screened using *E. coli*-absorbed autologous patient serum, as described in Sambrook et al., (*Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratories, Cold Spring Harbor, NY, 1989), with the secondary antibody being goat anti-human IgG-A-M (H + L) conjugated with alkaline phosphatase, developed with NBT/BCIP (Gibco BRL). Positive plaques expressing immunoreactive antigens were purified. Phagemid from the plaques was rescued and the nucleotide sequences of the clones was  
15  
20 determined.

Fifteen clones were isolated, referred to hereinafter as LT86-1 – LT86-15. The isolated cDNA sequences for LT86-1 – LT86-8 and LT86-10 - LT86-15 are provided in SEQ ID NO: 17-24 and 26-31, respectively, with the corresponding predicted amino acid sequences being provided in SEQ ID NO: 32-39 and 41-46, respectively. The determined cDNA sequence for LT86-9 is provided in SEQ ID NO: 25, with the corresponding predicted amino acid sequences from the 3' and 5' ends being provided in SEQ ID NO: 40 and 65, respectively. These sequences were compared to those in the gene bank as described above. Clones LT86-3, LT86-6 – LT86-9, LT86-11 – LT86-13 and LT86-15 (SEQ ID NO: 19, 22-25, 27-29 and 31, respectively) were found to show some homology to previously identified expressed sequence tags (ESTs), with clones LT86-6, LT86-8, LT86-11, LT86-12 and LT86-15  
25  
30

appearing to be similar or identical to each other. Clone LT86-3 was found to show some homology with a human transcription repressor. Clones LT86-6, 8, 9, 11, 12 and 15 were found to show some homology to a yeast RNA Pol II transcription regulation mediator. Clone LT86-13 was found to show some homology with a *C. elegans* leucine aminopeptidase. Clone LT86-9 appears to contain two inserts, with the 5' sequence showing homology to the previously identified antisense sequence of interferon alpha-induced P27, and the 3' sequence being similar to LT86-6. Clone LT86-14 (SEQ ID NO: 30) was found to show some homology to the trithorax gene and has an "RGD" cell attachment sequence and a beta-Lactamase A site which functions in hydrolysis of penicillin. Clones LT86-1, LT86-2, LT86-4, LT86-5 and LT86-10 (SEQ ID NOS: 17, 18, 20, 21 and 26, respectively) were found to show homology to previously identified genes. A subsequently determined extended cDNA sequence for LT86-4 is provided in SEQ ID NO: 66, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 67.

Subsequent studies led to the isolation of five additional clones, referred to as LT86-20, LT86-21, LT86-22, LT86-26 and LT86-27. The determined 5' cDNA sequences for LT86-20, LT86-22, LT86-26 and LT86-27 are provided in SEQ ID NO: 68 and 70-72, respectively, with the determined 3' cDNA sequences for LT86-21 being provided in SEQ ID NO: 69. The corresponding predicted amino acid sequences for LT86-20, LT86-21, LT86-22, LT86-26 and LT86-27 are provided in SEQ ID NO: 73-77, respectively. LT86-22 and LT86-27 were found to be highly similar to each other. Comparison of these sequences to those in the gene bank as described above, revealed no significant homologies to LT86-22 and LT86-27. LT86-20, LT86-21 and LT86-26 were found to show homology to previously identified genes.

In further studies, a cDNA expression library was prepared using mRNA from a lung small cell carcinoma cell line in the lambda ZAP Express expression vector (Stratagene), and screened as described above, with a pool of two lung small cell carcinoma patient sera. The sera pool was adsorbed with *E. coli* lysate and human PBMC lysate was added to the serum to block antibody to proteins found in normal tissue. Seventy-three clones were isolated. The determined cDNA sequences of these clones are provided in SEQ ID NO: 290-362. The sequences of SEQ ID NO: 289-292,

294, 296-297, 300, 302, 303, 305, 307-315, 317-320, 322-325, 327-332, 334, 335, 338-341, 343-352, 354-358, 360 and 362 were found to show some homology to previously isolated genes. The sequences of SEQ ID NO: 293, 295, 298, 299, 301, 304, 306, 316, 321, 326, 333, 336, 337, 342, 353, 359 and 361 were found to show some homology to  
5 previously identified ESTs.

## Example 3

USE OF MOUSE ANTISERA TO IDENTIFY DNA SEQUENCES ENCODING  
LUNG TUMOR ANTIGENS

This example illustrates the isolation of cDNA sequences encoding lung  
5 tumor antigens by screening of lung tumor cDNA libraries with mouse anti-tumor sera.

A directional cDNA lung tumor expression library was prepared as  
described above in Example 2. Sera was obtained from SCID mice containing late  
passaged human squamous cell and adenocarcinoma tumors. These sera were pooled  
and injected into normal mice to produce anti-lung tumor serum. Approximately  
10 200,000 PFUs were screened from the unamplified library using this antiserum. Using  
a goat anti-mouse IgG-A-M (H+L) alkaline phosphatase second antibody developed  
with NBT/BCIP (BRL Labs.), approximately 40 positive plaques were identified.  
Phage was purified and phagemid excised for 9 clones with inserts in a pBK-CMV  
vector for expression in prokaryotic or eukaryotic cells.

15 The determined cDNA sequences for 7 of the isolated clones (hereinafter  
referred to as L86S-3, L86S-12, L86S-16, L86S-25, L86S-36, L86S-40 and L86S-46)  
are provided in SEQ ID NO: 49-55, with the corresponding predicted amino acid  
sequences being provided in SEQ ID NO: 56-62, respectively. The 5' cDNA sequences  
for the remaining 2 clones (hereinafter referred to as L86S-30 and L86S-41) are  
20 provided in SEQ ID NO: 63 and 64. L86S-36 and L86S-46 were subsequently  
determined to represent the same gene. Comparison of these sequences with those in  
the public database as described above, revealed no significant homologies to clones  
L86S-30, L86S-36 and L86S-46 (SEQ ID NO: 63, 53 and 55, respectively). L86S-16  
(SEQ ID NO: 51) was found to show some homology to an EST previously identified in  
25 fetal lung and germ cell tumor. The remaining clones were found to show at least some  
degree of homology to previously identified human genes. Subsequently determined  
extended cDNA sequences for L86S-12, L86S-36 and L86S-46 are provided in SEQ ID  
NO: 78-80, respectively, with the corresponding predicted amino acid sequences being  
provided in SEQ ID NO: 81-83.

30 Subsequent studies led to the determination of 5' cDNA sequences for an  
additional nine clones, referred to as L86S-6, L86S-11, L86S-14, L86S-29, L86S-34,

L86S-39, L86S-47, L86S-49 and L86S-51 (SEQ ID NO: 84-92, respectively). The corresponding predicted amino acid sequences are provided in SEQ ID NO: 93-101, respectively. L86S-30, L86S-39 and L86S-47 were found to be similar to each other. Comparison of these sequences with those in the gene bank as described above, 5 revealed no significant homologies to L86S-14. L86S-29 was found to show some homology to a previously identified EST. L86S-6, L86S-11, L86S-34, L86S-39, L86S-47, L86S-49 and L86S-51 were found to show some homology to previously identified genes.

In further studies, a directional cDNA library was constructed using a 10 Stratagene kit with a Lambda Zap Express vector. Total RNA for the library was isolated from two primary squamous lung tumors and poly A+ RNA was isolated using an oligo dT column. Antiserum was developed in normal mice using a pool of sera from three SCID mice implanted with human squamous lung carcinomas. Approximately 700,000 PFUs were screened from the unamplified library with *E. coli* 15 absorbed mouse anti-SCID tumor serum. Positive plaques were identified as described above. Phage was purified and phagemid excised for 180 clones with inserts in a pBK-CMV vector for expression in prokaryotic or eukaryotic cells.

The determined cDNA sequences for 23 of the isolated clones are provided in SEQ ID NO: 126-148. Comparison of these sequences with those in the 20 public database as described above revealed no significant homologies to the sequences of SEQ ID NO: 139 and 143-148. The sequences of SEQ ID NO: 126-138 and 140-142 were found to show homology to previously identified human polynucleotide sequences.



## Example 4

USE OF MOUSE ANTISERA TO SCREEN LUNG TUMOR LIBRARIES  
PREPARED FROM SCID MICE

5 This example illustrates the isolation of cDNA sequences encoding lung tumor antigens by screening of lung tumor cDNA libraries prepared from SCID mice with mouse anti-tumor sera.

A directional cDNA lung tumor expression library was prepared using a Stratagene kit with a Lambda Zap Express vector. Total RNA for the library was taken  
10 from a late passaged lung adenocarcinoma grown in SCID mice. Poly A+ RNA was isolated using a Message Maker Kit (Gibco BRL). Sera was obtained from two SCID mice implanted with lung adenocarcinomas. These sera were pooled and injected into normal mice to produce anti-lung tumor serum. Approximately 700,000 PFUs were screened from the unamplified library with *E. coli*-absorbed mouse anti-SCID tumor  
15 serum. Positive plaques were identified with a goat anti-mouse IgG-A-M (H+L) alkaline phosphatase second antibody developed with NBT/BCIP (Gibco BRL). Phage was purified and phagemid excised for 100 clones with insert in a pBK-CMV vector for expression in prokaryotic or eukaryotic cells.

The determined 5' cDNA sequences for 33 of the isolated clones are  
20 provided in SEQ ID NO: 149-181. The corresponding predicted amino acid sequences for SEQ ID NO: 149, 150, 152-154, 156-158 and 160-181 are provided in SEQ ID NO: 182, 183, 186, 188-193 and 194-215, respectively. The clone of SEQ ID NO: 151 (referred to as SAL-25) was found to contain two open reading frames (ORFs). The predicted amino acid sequences encoded by these ORFs are provided in SEQ ID NO:  
25 184 and 185. The clone of SEQ ID NO: 153 (referred to as SAL-50) was found to contain two open reading frames encoding the predicted amino acid sequences of SEQ ID NO: 187 and 216. Similarly, the clone of SEQ ID NO: 155 (referred to as SAL-66) was found to contain two open reading frames encoding the predicted amino acid sequences of SEQ ID NO: 189 and 190. Comparison of the isolated sequences with  
30 those in the public database revealed no significant homologies to the sequences of SEQ ID NO: 151, 153 and 154. The sequences of SEQ ID NO: 149, 152, 156, 157 and 158

were found to show some homology to previously isolated expressed sequence tags (ESTs). The sequences of SEQ ID NO: 150, 155 and 159-181 were found to show homology to sequences previously identified in humans.

Using the procedures described above, two directional cDNA libraries  
5 (referred to as LT46-90 and LT86-21) were prepared from two late passaged lung squamous carcinomas grown in SCID mice and screened with sera obtained from SCID mice implanted with human squamous lung carcinomas. The determined cDNA sequences for the isolated clones are provided in SEQ ID NO: 217-237 and 286-289. SEQ ID NO: 286 was found to be a longer sequence of LT4690-71 (SEQ ID NO: 237).  
10 Comparison of these sequences with those in the public databases revealed no known homologies to the sequences of SEQ ID NO: 219, 220, 225, 226, 287 and 288. The sequences of SEQ ID NO: 218, 221, 222 and 224 were found to show some homology to previously identified sequences of unknown function. The sequence of SEQ ID NO: 236 was found to show homology to a known mouse mRNA sequence. The sequences  
15 of SEQ ID NO: 217, 223, 227-237, 286 and 289 showed some homology to known human DNA and/or RNA sequences.

In further studies using the techniques described above, one of the cDNA libraries described above (LT86-21) was screened with *E. coli*-absorbed mouse anti-SCID tumor serum. This serum was obtained from normal mice immunized with a pool  
20 of 3 sera taken from SCID mice implanted with human squamous lung carcinomas. The determined cDNA sequences for the isolated clones are provided in SEQ ID NO: 238-285. Comparison of these sequences with those in the public databases revealed no significant homologies to the sequences of SEQ ID NO: 253, 260, 277 and 285. The sequences of SEQ ID NO: 249, 250, 256, 266, 276 and 282 were found to show some  
25 homology to previously isolated expressed sequence tags (ESTs). The sequences of SEQ ID NO: 238-248, 251, 252, 254, 255, 257-259, 261-263, 265, 267-275, 278-281, 283 and 284 were found to show some homology to previously identified DNA or RNA sequences.

Example 5DETERMINATION OF TISSUE SPECIFICITY OF LUNG TUMOR  
POLYPEPTIDES

Using gene specific primers, mRNA expression levels for representative  
5 lung tumor polypeptides were examined in a variety of normal and tumor tissues using  
RT-PCR.

Briefly, total RNA was extracted from a variety of normal and tumor  
tissues using Trizol reagent. First strand synthesis was carried out using 2 µg of total  
RNA with SuperScript II reverse transcriptase (BRL Life Technologies) at 42 °C for  
10 one hour. The cDNA was then amplified by PCR with gene-specific primers. To  
ensure the semi-quantitative nature of the RT-PCR, β-actin was used as an internal  
control for each of the tissues examined. 1 µl of 1:30 dilution of cDNA was employed  
to enable the linear range amplification of the β-actin template and was sensitive  
enough to reflect the differences in the initial copy numbers. Using these conditions,  
15 the β-actin levels were determined for each reverse transcription reaction from each  
tissue. DNA contamination was minimized by DNase treatment and by assuring a  
negative PCR result when using first strand cDNA that was prepared without adding  
reverse transcriptase.

mRNA Expression levels were examined in five different types of tumor  
20 tissue (lung squamous tumor from 3 patients, lung adenocarcinoma, prostate tumor,  
colon tumor and lung tumor), and different normal tissues, including lung from four  
patients, prostate, brain, kidney, liver, ovary, skeletal muscle, skin, small intestine,  
myocardium, retina and testes. L86S-46 was found to be expressed at high levels in  
lung squamous tumor, colon tumor and prostate tumor, and was undetectable in the  
25 other tissues examined. L86S-5 was found to be expressed in the lung tumor samples  
and in 2 out of 4 normal lung samples, but not in the other normal or tumor tissues  
tested. L86S-16 was found to be expressed in all tissues except normal liver and normal  
stomach. Using real-time PCR, L86S-46 was found to be over-expressed in lung  
squamous tissue and normal tonsil, with expression being low or undetectable in all  
30 other tissues examined.

Example 6

## ISOLATION OF DNA SEQUENCES ENCODING LUNG TUMOR ANTIGENS

DNA sequences encoding antigens potentially involved in squamous cell  
5 lung tumor formation were isolated as follows.

A lung tumor directional cDNA expression library was constructed employing the Lambda ZAP Express expression system (Stratagene, La Jolla, CA). Total RNA for the library was taken from a pool of two human squamous epithelial lung carcinomas and poly A+ RNA was isolated using oligo-dT cellulose (Gibco BRL,  
10 Gaithersburg, MD). Phagemid were rescued at random and the cDNA sequences of isolated clones were determined.

The determined cDNA sequence for the clone SLT-T1 is provided in SEQ ID NO: 102, with the determined 5' cDNA sequences for the clones SLT-T2, SLT-T3, SLT-T5, SLT-T7, SLT-T9, SLT-T10, SLT-T11 and SLT-T12 being provided  
15 in SEQ ID NO: 103-110, respectively. The corresponding predicted amino acid sequence for SLT-T1, SLT-T2, SLT-T3, SLT-T10 and SLT-T12 are provided in SEQ ID NO: 111-115, respectively. Comparison of the sequences for SLT-T2, SLT-T3, SLT-T5, SLT-T7, SLT-T9 and SLT-T11 with those in the public databases as described above, revealed no significant homologies. The sequences for SLT-T10 and SLT-T12  
20 were found to show some homology to sequences previously identified in humans.

The sequence of SLT-T1 was determined to show some homology to a PAC clone of unknown protein function. The cDNA sequence of SLT-T1 (SEQ ID NO: 102) was found to contain a mutator (MUTT) domain. Such domains are known to function in removal of damaged guanine from DNA that can cause A to G transversions  
25 (see, for example, el-Deiry, W.S., 1997 *Curr. Opin. Oncol.* 9:79-87; Okamoto, K. et al. 1996 *Int. J. Cancer* 65:437-41; Wu, C. et al. 1995 *Biochem. Biophys. Res. Commun.* 214:1239-45; Porter, D.W. et al. 1996 *Chem. Res. Toxicol.* 9:1375-81). SLT-T1 may thus be of use in the treatment, by gene therapy, of lung cancers caused by, or associated with, a disruption in DNA repair.

30 In further studies, DNA sequences encoding antigens potentially involved in adenocarcinoma lung tumor formation were isolated as follows. A human

lung tumor directional cDNA expression library was constructed employing the Lambda ZAP Express expression system (Stratagene, La Jolla, CA). Total RNA for the library was taken from a late SCID mouse passaged human adenocarcinoma and poly A+ RNA was isolated using the Message Maker kit (Gibco BRL, Gaithersburg, MD).  
5 Phagemid were rescued at random and the cDNA sequences of isolated clones were determined.

The determined 5' cDNA sequences for five isolated clones (referred to as SALT-T3, SALT-T4, SALT-T7, SALT-T8, and SALT-T9) are provided in SEQ ID NO: 116-120, with the corresponding predicted amino acid sequences being provided in  
10 SEQ ID NO: 121-125. SALT-T3 was found to show 98% identity to the previously identified human transducin-like enhancer protein TLE2. SALT-T4 appears to be the human homologue of the mouse H beta 58 gene. SALT-T7 was found to have 97% identity to human 3-mercaptopyruvate sulfurtransferase and SALT-T8 was found to show homology to human interferon-inducible protein 1-8U. SALT-T9 shows  
15 approximately 90% identity to human mucin MUC 5B.

cDNA sequences encoding antigens potentially involved in small cell lung carcinoma development were isolated as follows. cDNA expression libraries were constructed with mRNA from the small cell lung carcinoma cell lines NCIH69, NCIH128 and DMS79 (all available from the American Type Culture Collection,  
20 Manassas, VA) employing the Lambda ZAP Express expression system (Stratagene, La Jolla, CA). Phagemid were rescued at random and the cDNA sequences of 27 isolated clones were determined. Comparison of the determined cDNA sequences revealed no significant homologies to the sequences of SEQ ID NO: 372 and 373. The sequences of SEQ ID NO: 364, 369, 377, 379 and 386 showed some homology to previously isolated  
25 ESTs. The sequences of the remaining 20 clones showed some homology to previously identified genes. The cDNA sequences of these clones are provided in SEQ ID NO: 363, 365-368, 370, 371, 374-376, 378, 380-385 and 387-389, wherein SEQ ID NO: 363, 366-368, 370, 375, 376, 378, 380-382, 384 and 385 are full-length sequences.

Example 7

## SYNTHESIS OF POLYPEPTIDES

Polypeptides may be synthesized on a Perkin Elmer/Applied Biosystems  
5 Division 430A peptide synthesizer using Fmoc chemistry with HPTU (O-Benzotriazole-N,N,N',N'-tetramethyluronium hexafluorophosphate) activation. A Gly-Cys-Gly sequence may be attached to the amino terminus of the peptide to provide a method of conjugation, binding to an immobilized surface, or labeling of the peptide. Cleavage of the peptides from the solid support may be carried out using the following  
10 cleavage mixture: trifluoroacetic acid:ethanedithiol:thioanisole:water:phenol (40:1:2:2:3). After cleaving for 2 hours, the peptides may be precipitated in cold methyl-t-butyl-ether. The peptide pellets may then be dissolved in water containing 0.1% trifluoroacetic acid (TFA) and lyophilized prior to purification by C18 reverse phase HPLC. A gradient of 0%-60% acetonitrile (containing 0.1% TFA) in water  
15 (containing 0.1% TFA) may be used to elute the peptides. Following lyophilization of the pure fractions, the peptides may be characterized using electrospray or other types of mass spectrometry and by amino acid analysis.

Example 820 ISOLATION AND CHARACTERIZATION OF DNA SEQUENCES ENCODING  
LUNG TUMOR ANTIGENS BY T-CELL EXPRESSION CLONING

Lung tumor antigens may also be identified by T cell expression cloning. One source of tumor specific T cells is from surgically excised tumors from human  
25 patients.

A non-small cell lung carcinoma was minced and enzymatically digested for several hours to release tumor cells and infiltrating lymphocytes (tumor infiltrating T cells, or TILs). The cells were washed in HBSS buffer and passed over a Ficoll (100%/75%/HBSS) discontinuous gradient to separate tumor cells and lymphocytes  
30 from non-viable cells. Two bands were harvested from the interfaces; the upper band at the 75%/HBSS interface contained predominantly tumor cells, while the lower band at



the 100%/75%/HBSS interface contained a majority of lymphocytes. The TILs were expanded in culture, either in 24-well plates with culture media supplemented with 10 ng/ml IL-7 and 100 U/ml IL-2, or alternatively, 24-well plates that have been pre-coated with the anti-CD3 monoclonal antibody OKT3. The resulting TIL cultures were analyzed by FACS to confirm that a high percentage were CD8+ T cells (>90% of gated population) with only a small percentage of CD4+ cells.

In addition, non-small cell lung carcinoma cells were expanded in culture using standard techniques to establish a tumor cell line, which was later confirmed to be a lung carcinoma cell line by immunohistochemical analysis. This tumor cell line was transduced with a retroviral vector to express human CD80, and characterized by FACS analysis to confirm high expression levels of CD80, and class I and II MHC molecules.

The specificity of the TIL lines to lung tumor was confirmed by INF- $\gamma$  and/or TNF- $\alpha$  cytokine release assays. TIL cells from day 21 cultures were co-cultured with either autologous or allogeneic tumor cells, EBV-immortalized LCL, or control cell lines Daudi and K562, and the culture supernatant monitored by ELISA for the presence of cytokines. The TIL specifically recognized autologous tumor but not allogeneic tumor. In addition, there was no recognition of EBV-immortalized LCL or the control cell lines, indicating that the TIL lines are tumor specific and are potentially recognizing a tumor antigen presented by autologous MHC molecules.

The characterized tumor-specific TIL lines were expanded to suitable numbers for T cell expression cloning using soluble anti-CD3 antibody in culture with irradiated EBV transformed LCLs and PBL feeder cells in the presence of 20 U/ml IL-2. Clones from the expanded TIL lines were generated by standard limiting dilution techniques. Specifically, TIL cells were seeded at 0.5 cells/well in a 96-well U bottom plate and stimulated with CD-80-transduced autologous tumor cells, EBV transformed LCL, and PBL feeder cells in the presence of 50 U/ml IL-2. These clones were further analyzed for tumor specificity by  $^{51}\text{Cr}$  microcytotoxicity and IFN- $\gamma$  bioassays. The MHC restriction element recognized by the TIL clones may be determined by antibody blocking studies.

CTL lines or clones prepared as described above may be employed to

identify tumor specific antigens. For example, autologous fibroblasts or LCL from a patient may be transfected or transduced with polynucleotide fragments derived from a lung tumor cDNA library to generate target cells expressing tumor polypeptides. The target cells expressing tumor polypeptides in the context of MHC will be recognized by the CTL line or clone, resulting in T-cell activation which can be monitored by cytokine detection assays. The tumor gene being expressed by the target cell and recognized by the tumor-specific CTL may then be isolated.

From the foregoing, it will be appreciated that, although specific embodiments of the invention have been described herein for the purposes of illustration, various modifications may be made without deviating from the spirit and scope of the invention.

Claims

1. An isolated polypeptide, comprising at least an immunogenic portion of a lung tumor protein, or a variant thereof, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence  
5 selected from the group consisting of:
- (a) sequences recited in SEQ ID NOs: 2, 8, 15, 16, 22, 24, 30, 32-34, 36, 38, 40, 41, 46-49, 52, 54, 59, 60, 65-69, 79, 89, 90, 93, 99-101, 109-111, 116-119, 123-132, 138-142, 143, 148, 149, 156, 168, 170-182, 184, 189, 191-193, 196, 205, 207, 210-212, 214, 215, 218, 224-226, 228, 233, 234, 236, 238, 241, 242, 245, 246, 248, 250, 253, 254, 256, 259, 260, 262, 263, 266, 267, 270-273, 279, 282, 291, 293, 294, 298, 300, 302, 303, 310-313, 315, 317, 320, 322, 324, 332-335, 345, 347, 356, 358, 361, 362, 366, 369, 371-378, 380-404, 406, 409-417, 419-423, 425, 427-429, 433-436, 438-441, 443, 446-451, 454, 455, 457-461, 476, 477, 479, 483, 488, 491, 492, 497, 498, 500, 510, 519, 527, 528, 543, 545, 547, 553, 556, 559, 561, 564, 565, 568, 569, 574-577, 579, 580, 584, 585, 587, 592, 595, 598, 603, 608, 610, 613, 621-623, 626, 642, 648 and 668;  
10
- (b) sequences that hybridize to a sequence recited in any one of SEQ ID NOs: 2, 8, 15, 16, 22, 24, 30, 32-34, 36, 38, 40, 41, 46-49, 52, 54, 59, 60, 65-69, 79, 89, 90, 93, 99-101, 109-111, 116-119, 123-132, 138-142, 143, 148, 149, 156, 168, 170-182, 184, 189, 191-193, 196, 205, 207, 210-212, 214, 215, 218, 224-226, 228, 233, 234, 236, 238, 241, 242, 245, 246, 248, 250, 253, 254, 256, 259, 260, 262, 263, 266, 267, 270-273, 279, 282, 291, 293, 294, 298, 300, 302, 303, 310-313, 315, 317, 320, 322, 324, 332-335, 345, 347, 356, 358, 361, 362, 366, 369, 371-378, 380-404, 406, 409-417, 419-423, 425, 427-429, 433-436, 438-441, 443, 446-451, 454, 455, 457-461, 476, 477, 479, 483, 488, 491, 492, 497, 498, 500, 510, 519, 527, 528, 543, 545, 547, 553, 556, 559, 561, 564, 565, 568, 569, 574-577, 579, 580, 584, 585, 587, 592, 595, 598, 603, 608, 610, 613, 621-623, 626, 642, 648 and 668  
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under moderately stringent conditions; and  
(c) complements of sequences of (a) or (b).

2. An isolated polypeptide according to claim 1, wherein the  
5 polypeptide comprises an amino acid sequence that is encoded by a polynucleotide  
sequence recited in any one of SEQ ID NOs: 218-222, 224-226, 249, 250, 253, 256,  
266, 276, 277, 282, 285, 293, 295, 298, 299, 301, 304, 306, 316, 321, 326, 333, 336,  
337, 342, 353, 359, 361, 364, 369, 372, 373, 377, 379 and 386, or a complement of any  
of the foregoing polynucleotide sequences.

10 3. An isolated polynucleotide encoding at least 15 amino acid  
residues of a lung tumor protein, or a variant thereof that differs in one or more  
substitutions, deletions, additions and/or insertions such that the ability of the variant to  
react with antigen-specific antisera is not substantially diminished, wherein the tumor  
protein comprises an amino acid sequence that is encoded by a polynucleotide  
15 comprising a sequence recited in any one of SEQ ID Nos: 218-222, 224-226, 249, 250,  
253, 256, 266, 276, 277, 282, 285, 293, 295, 298, 299, 301, 304, 306, 316, 321, 326,  
333, 336, 337, 342, 353, 359, 361, 364, 369, 372, 373, 377, 379 and 386, or a  
complement of any of the foregoing sequences.

20 4. An isolated polynucleotide encoding a lung tumor protein, or a  
variant thereof, wherein the tumor protein comprises an amino acid sequence that is  
encoded by a polynucleotide comprising a sequence recited in any one of SEQ ID  
NOs: 218-222, 224-226, 249, 250, 253, 256, 266, 276, 277, 282, 285, 293, 295, 298,  
299, 301, 304, 306, 316, 321, 326, 333, 336, 337, 342, 353, 359, 361, 364, 369, 372,  
25 373, 377, 379 and 386, or a complement of any of the foregoing sequences.

5. An isolated polynucleotide, comprising a sequence recited in any  
one of SEQ ID NOs: 218-222, 224-226, 249, 250, 253, 256, 266, 276, 277, 282, 285,  
293, 295, 298, 299, 301, 304, 306, 316, 321, 326, 333, 336, 337, 342, 353, 359, 361,  
30 364, 369, 372, 373, 377, 379 and 386.

6. An isolated polynucleotide, comprising a sequence that hybridizes to a sequence recited in any one of SEQ ID NOs: 218-222, 224-226, 249, 250, 253, 256, 266, 276, 277, 282, 285, 293, 295, 298, 299, 301, 304, 306, 316, 321, 326, 333, 336, 337, 342, 353, 359, 361, 364, 369, 372, 373, 377, 379 and 386 under moderately stringent conditions.

7. An isolated polynucleotide complementary to a polynucleotide according to any one of claims 3-6.

10

8. An expression vector, comprising a polynucleotide according to any one of claims 3-8.

9. A host cell transformed or transfected with an expression vector according to claim 8.

10. An isolated antibody, or antigen-binding fragment thereof, that specifically binds to a lung tumor protein that comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOs: 218-222, 224-226, 249, 250, 253, 256, 266, 276, 277, 282, 285, 293, 295, 298, 299, 301, 304, 306, 316, 321, 326, 333, 336, 337, 342, 353, 359, 361, 364, 369, 372, 373, 377, 379 and 386, or a complement of any of the foregoing polynucleotide sequences.

11. A fusion protein, comprising at least one polypeptide according to claim 1.

12. A fusion protein according to claim 11, wherein the fusion protein comprises an expression enhancer that increases expression of the fusion protein in a host cell transfected with a polynucleotide encoding the fusion protein.

30

13. A fusion protein according to claim 11, wherein the fusion

protein comprises a T helper epitope that is not present within the polypeptide of claim 1.

14. A fusion protein according to claim 11, wherein the fusion  
5 protein comprises an affinity tag.

15. An isolated polynucleotide encoding a fusion protein according  
to claim 11.

10 16. A pharmaceutical composition, comprising a physiologically  
acceptable carrier and at least one component selected from the group consisting of:

- (a) a polypeptide according to claim 1;
- (b) a polynucleotide according to claim 3;
- (c) an antibody according to claim 10;
- 15 (d) a fusion protein according to claim 11; and
- (e) a polynucleotide according to claim 15.

17. A vaccine comprising an immunostimulant and at least one  
component selected from the group consisting of:

- 20 (a) a polypeptide according to claim 1;
- (b) a polynucleotide according to claim 3;
- (c) an antibody according to claim 10;
- (d) a fusion protein according to claim 11; and
- (e) a polynucleotide according to claim 15.

25

18. A vaccine according to claim 17, wherein the immunostimulant  
is an adjuvant.

19. A vaccine according to any claim 17, wherein the  
30 immunostimulant induces a predominantly Type I response.



20. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a pharmaceutical composition according to claim 16.

5 21. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a vaccine according to claim 17.

10 22. A pharmaceutical composition comprising an antigen-presenting cell that expresses a polypeptide according to claim 1, in combination with a pharmaceutically acceptable carrier or excipient.

15 23. A pharmaceutical composition according to claim 22, wherein the antigen presenting cell is a dendritic cell or a macrophage.

24. A vaccine comprising an antigen-presenting cell that expresses a polypeptide comprising at least an immunogenic portion of a lung tumor protein, or a variant thereof, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:

- 20 (a) sequences recited in SEQ ID NOs: 217-389;  
(b) sequences that hybridize to a sequence recited in any one of SEQ ID NOs: 217-389 under moderately stringent conditions; and  
(c) complements of sequences of (i) or (ii);  
in combination with an immunostimulant.

25 25. A vaccine according to claim 24, wherein the immunostimulant is an adjuvant.

30 26. A vaccine according to claim 24, wherein the immunostimulant induces a predominantly Type I response.

27. A vaccine according to claim 24, wherein the antigen-presenting cell is a dendritic cell.

28. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of an antigen-presenting cell that expresses a polypeptide comprising at least an immunogenic portion of a lung tumor protein, or a variant thereof, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:

- (a) sequences recited in SEQ ID NOs: 217-389;
  - (b) sequences that hybridize to a sequence recited in any one of SEQ ID NOs: 217-389 under moderately stringent conditions; and
  - (c) complements of sequences of (i) or (ii) encoded by a polynucleotide recited in any one of SEQ ID NOs: 217-389;
- and thereby inhibiting the development of a cancer in the patient.

29. A method according to claim 28, wherein the antigen-presenting cell is a dendritic cell.

30. A method according to any one of claims 20, 21 and 28, wherein the cancer is lung cancer.

31. A method for removing tumor cells from a biological sample, comprising contacting a biological sample with T cells that specifically react with a lung tumor protein, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:

- (i) polynucleotides recited in any one of SEQ ID NOs: 217-389; and
- (ii) complements of the foregoing polynucleotides;

wherein the step of contacting is performed under conditions and for a time sufficient to permit the removal of cells expressing the antigen from the sample.

32. A method according to claim 31, wherein the biological sample is blood or a fraction thereof.

5 33. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient a biological sample treated according to the method of claim 31.

10 34. A method for stimulating and/or expanding T cells specific for a lung tumor protein, comprising contacting T cells with at least one component selected from the group consisting of:

15 (a) polypeptides comprising at least an immunogenic portion of a lung tumor protein, or a variant thereof, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:

(i) sequences recited in SEQ ID NOs: 217-389;

(ii) sequences that hybridize to a sequence recited in any one of SEQ ID NOs: 217-389 under moderately stringent conditions; and

(iii) complements of sequences of (i) or (ii);

20 (b) polynucleotides encoding a polypeptide of (a); and

(c) antigen presenting cells that express a polypeptide of (a);

under conditions and for a time sufficient to permit the stimulation and/or expansion of T cells.

25 35. An isolated T cell population, comprising T cells prepared according to the method of claim 34.

30 36. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a T cell population according to claim 35.

37. A method for inhibiting the development of a cancer in a patient, comprising the steps of:

(a) incubating CD4<sup>+</sup> and/or CD8<sup>+</sup> T cells isolated from a patient with at least one component selected from the group consisting of:

5 (i) polypeptides comprising at least an immunogenic portion of a lung tumor protein, or a variant thereof, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:

(1) sequences recited in SEQ ID NOs: 217-389;  
10 (2) sequences that hybridize to a sequence recited in any one of SEQ ID NOs: 217-389 under moderately stringent conditions; and

(3) complements of sequences of (1) or (2);  
(ii) polynucleotides encoding a polypeptide of (i); and  
15 (iii) antigen presenting cells that expresses a polypeptide of (i);

such that T cells proliferate; and

(b) administering to the patient an effective amount of the proliferated T cells, and thereby inhibiting the development of a cancer in the patient.

20

38. A method for inhibiting the development of a cancer in a patient, comprising the steps of:

(a) incubating CD4<sup>+</sup> and/or CD8<sup>+</sup> T cells isolated from a patient with at least one component selected from the group consisting of:

25 (i) polypeptides comprising at least an immunogenic portion of a lung tumor protein, or a variant thereof, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:

(1) sequences recited in SEQ ID NOs: 217-389;  
30 (2) sequences that hybridize to a sequence recited in any one of SEQ ID NOs: 217-389 under moderately stringent conditions;

and

- (3) complements of sequences of (1) or (2);
- (ii) polynucleotides encoding a polypeptide of (i); and
- (iii) antigen presenting cells that express a polypeptide

5 of (i);

such that T cells proliferate;

- (b) cloning at least one proliferated cell to provide cloned T cells;

and

- (c) administering to the patient an effective amount of the cloned
- 10 T cells, and thereby inhibiting the development of a cancer in the patient.

39. A method for determining the presence or absence of a cancer in a patient, comprising the steps of:

- (a) contacting a biological sample obtained from a patient with a
- 15 binding agent that binds to a lung tumor protein, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOs: 217-389 or a complement of any of the foregoing polynucleotide sequences;

- (b) detecting in the sample an amount of polypeptide that binds to
- 20 the binding agent; and

- (c) comparing the amount of polypeptide to a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient.

40. A method according to claim 39, wherein the binding agent is an

25 antibody.

41. A method according to claim 42, wherein the antibody is a monoclonal antibody.

30 42. A method according to claim 39, wherein the cancer is lung cancer.

43. A method for monitoring the progression of a cancer in a patient, comprising the steps of:

5 (a) contacting a biological sample obtained from a patient at a first point in time with a binding agent that binds to a lung tumor protein, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOs: 217-389 or a complement of any of the foregoing polynucleotide sequences;

10 (b) detecting in the sample an amount of polypeptide that binds to the binding agent;

(c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and

15 (d) comparing the amount of polypeptide detected in step (c) to the amount detected in step (b) and therefrom monitoring the progression of the cancer in the patient.

44. A method according to claim 43, wherein the binding agent is an antibody.

20 45. A method according to claim 44, wherein the antibody is a monoclonal antibody.

46. A method according to claim 43, wherein the cancer is a lung cancer.

25

47. A method for determining the presence or absence of a cancer in a patient, comprising the steps of:

30 (a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide that encodes a lung tumor protein, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOs: 217-389 or a complement



of any of the foregoing polynucleotide sequences;

(b) detecting in the sample an amount of a polynucleotide that hybridizes to the oligonucleotide; and

(c) comparing the amount of polynucleotide that hybridizes to the oligonucleotide to a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient.

48. A method according to claim 47, wherein the amount of polynucleotide that hybridizes to the oligonucleotide is determined using a polymerase chain reaction.

49. A method according to claim 47, wherein the amount of polynucleotide that hybridizes to the oligonucleotide is determined using a hybridization assay.

50. A method for monitoring the progression of a cancer in a patient, comprising the steps of:

(a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide that encodes a lung tumor protein, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOs: 217-389 or a complement of any of the foregoing polynucleotide sequences;

(b) detecting in the sample an amount of a polynucleotide that hybridizes to the oligonucleotide;

(c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and

(d) comparing the amount of polynucleotide detected in step (c) to the amount detected in step (b) and therefrom monitoring the progression of the cancer in the patient.

51. A method according to claim 50, wherein the amount of

polynucleotide that hybridizes to the oligonucleotide is determined using a polymerase chain reaction.

52. A method according to claim 50, wherein the amount of  
5 polynucleotide that hybridizes to the oligonucleotide is determined using a hybridization assay.

53. A diagnostic kit, comprising:  
(a) one or more antibodies according to claim 10; and  
10 (b) a detection reagent comprising a reporter group.

54. A kit according to claim 53, wherein the antibodies are immobilized on a solid support.

15 55. A kit according to claim 53, wherein the detection reagent comprises an anti-immunoglobulin, protein G, protein A or lectin.

56. A kit according to claim 53, wherein the reporter group is selected from the group consisting of radioisotopes, fluorescent groups, luminescent  
20 groups, enzymes, biotin and dye particles.

57. An oligonucleotide comprising 10 to 40 contiguous nucleotides that hybridize under moderately stringent conditions to a polynucleotide that encodes a lung tumor protein, wherein the tumor protein comprises an amino acid sequence that is  
25 encoded by a polynucleotide sequence recited in any one of SEQ ID NOs: 218-222, 224-226, 249, 250, 253, 256, 266, 276, 277, 282, 285, 293, 295, 298, 299, 301, 304, 306, 316, 321, 326, 333, 336, 337, 342, 353, 359, 361, 364, 369, 372, 373, 377, 379 and 386, or a complement of any of the foregoing polynucleotides.

30 58. A oligonucleotide according to claim 57, wherein the oligonucleotide comprises 10-40 contiguous nucleotides recited in any one of SEQ ID

NOs: 218-222, 224-226, 249, 250, 253, 256, 266, 276, 277, 282, 285, 293, 295, 298, 299, 301, 304, 306, 316, 321, 326, 333, 336, 337, 342, 353, 359, 361, 364, 369, 372, 373, 377, 379 and 386.

- 5                    59.    A diagnostic kit, comprising:
- (a)    an oligonucleotide according to claim 58; and
  - (b)    a diagnostic reagent for use in a polymerase chain reaction or hybridization assay.

## SEQUENCE LISTING

<110> Corixa Corporation  
 Reed, Steven G.  
 Lodes, Michael J.  
 Mohamath, Raodoh  
 Secrist, Heather

<120> COMPOUNDS FOR THERAPY AND DIAGNOSIS OF  
 LUNG CANCER AND METHODS FOR THEIR USE

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<210> 15  
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 <223> n = A,T,C or G

&lt;400&gt; 15

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<210> 16  
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 <213> Homo sapien  
  
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 <221> misc\_feature  
 <222> (1)...(522)  
 <223> n = A,T,C or G

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&lt;210&gt; 17

&lt;211&gt; 317

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 17

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&lt;210&gt; 18

&lt;211&gt; 392

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 18

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&lt;210&gt; 19

&lt;211&gt; 2624

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 19

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&lt;210&gt; 20

&lt;211&gt; 488

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 20

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&lt;210&gt; 21

&lt;211&gt; 391

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 21

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&lt;210&gt; 22

&lt;211&gt; 1320

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 22

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&lt;210&gt; 23

&lt;211&gt; 633

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 23

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 <212> DNA  
 <213> Homo sapien

<400> 24

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 <212> DNA  
 <213> Homo sapien

<400> 25

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&lt;210&gt; 26

&lt;211&gt; 493

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 26

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&lt;210&gt; 27

&lt;211&gt; 1331

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 27

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aacatgtaat	aatgaagtgg	tcaaaatgca	gaggctaaca	ttagaacact	tgaatcagat	180
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gcaacagecg	cagtcacctg	cccaagtatt	cccactagct	gattactata	tcattgctgg	300
agtgatctat	caggcaccag	acttgggata	agttataaac	tctagagtgc	ttactgcagt	360
gcatggtatt	cagtcagctt	ttgatgaagc	tatgtcatac	tgtcgatata	atccttccaa	420
aggggtattgg	tggcacttca	aagatcatga	agagcaagat	aaagtcagac	ctaaagccaa	480
aaggaaagaa	gaaccaagct	ctatttttca	gagacaacgt	gtggatgctt	tactttttaga	540
cctcagacaa	aaatttccac	ccaaatttgt	gcagctaaag	cctggagaaa	agcctgttcc	600
agtggatcaa	acaaagaaag	aggcagaacc	tataccagaa	actgtaaaac	ctgaggagaa	660
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gagacttcag	tgagtactgg	acaaaagaga	agcctggaag	actcctcatg	ctagttatca	780
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tgaccaatat	ggtgaaaccc	cgtctctact	aaaaatacaa	aaattagccg	ggcgtgggtgg	1020
cgggcgccca	tagtcccagc	tactcgggag	gctgagacag	gagacttgct	tgaacccggg	1080
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gagactttgt	ctcaaaaaaa	gaagaaaaga	tattattccc	atcatgattt	cttgtgaata	1200
tttgttatat	gtcttctgta	acctttcctc	tcccggactt	gagcaacctc	cacactcaca	1260

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 aaaaactcga g 1331

<210> 28  
 <211> 1333  
 <212> DNA  
 <213> Homo sapien

<400> 28  
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 acagaacatg taataatgaa gtggtcaaaa tgcagaggct aacattagaa cacttgaatc 180  
 agatgggttg aatcgagtac atccttttgc atgctcaaga gcccattctt ttcattcattc 240  
 ggaagcaaca gcggcagtc cctgcccag ttatcccact agctgattac tatatcattg 300  
 ctggagtgat ctatcaggca ccagacttgg gatcagttat aaactctaga gtgcttactg 360  
 cagtgcattg tattcagtc gcttttgatg aagctatgtc atactgtcga tatcatcctt 420  
 ccaaagggtg ttggtggcac ttcaaagatc atgaagagca agataaagtc agacctaaag 480  
 ccaaaaggaa agaagaacca agctctatct ttcagagaca acgtgtggat gctttacttt 540  
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 ggatgagact tcagtgagta ctggacaaaa gagaagcctg gaagactcct catgctagtt 780  
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 gtatggaatg cgcttatttt ttgaaaggat attaggccgg atgtgggtggc tcacgcctgt 900  
 aatcccagca ctttggggagg ccatggcggg tggatcactt gaggtcagaa gttcaagacc 960  
 agcctgacca atatggtgaa accccgtctc tactaaaaat acaaaaatta gccgggctgt 1020  
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 cgggaggtgg aggttgccct gagctgatta tcatgctgtt gcactccagc ttgggcgaca 1140  
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 atatttgtga tatgtcttct gtaacctttc ctctcccga cttgagcaac ctacacactc 1260  
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 aaaaaaactc gag 1331

<210> 29  
 <211> 813  
 <212> DNA  
 <213> Homo sapien

<400> 29  
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 actggcccgg ggtctgggtc cacctggaca tcgctgctcc agtgcattgt ggcgagcgag 180  
 ccacaggctt tggggtggct ctctacttgg ctcttttttg ccgtgcctcc gaggaccctg 240  
 tgctgaacct ggtatccccg ctggactgtg aggtggatgc ccaggaaggc gacaacatgg 300  
 ggcgtgactc caagagacgg aggtcgtgt gagggctact tcccagctgg tgacacaggg 360  
 ttecttacct cattttgcac tgactgattt taagcaattg aaagattaac taactcttaa 420  
 gatgagtttg gcttctcctt ctgtgcccag tggtgacagg agtgagccat tcttctctta 480  
 gaagcagctt aggggcttgg tggggtctgg agaaaattgt cacagacccc ataggtctcc 540  
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 ctgtagtgag tgtacttcct gaccagggc cttgctcaag ctggggctcc ctggggtgtc 660  
 taaccagccc tgggtagatg tgactggctg ttagggaccc cattctgtga agcaggagac 720  
 cctcacagct cccaccaacc ccagttcac ttgaagttga attaaatat gccacaacat 780  
 aaaaaaaaaa aaaaaaaaaa aaaaaaactc gag 813

<210> 30

&lt;211&gt; 1316

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 30

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cagtccaatc	atagaaaaga	tggaaaaaag	gacatgtgcc	ctgtgccctg	aaggccacga	120
gtggagtcaa	atatactttt	caccatcagg	aaatatagtt	gctcatgaaa	actgtttgct	180
gtattcatca	ggactgggtg	agtgtgagac	tcttgatcta	cgtaatacaa	ttagaaactt	240
tgatgtcaaa	tctgtaaaga	aagagatctg	gagaggaaga	agattgaaat	gctcattctg	300
taacaaagga	ggcgccaccg	tgggggtgtga	tttatgggtc	tgtaagaaga	gttaccacta	360
tgtctgtgcc	aaaaaggacc	aagcaattct	tcaagttgat	ggaaaccatg	gaacttacia	420
attattttgc	ccagaacatt	ctccagaaca	agaagaggcc	actgaaagtg	ctgatgaccc	480
aagcatgaag	aagaagagag	gaaaaaacia	acgcctctca	tcaggccctc	ctgcacagcc	540
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agatgcagct	gtcaaattct	cttttcttaa	gaaatgccag	gaagcaggac	ttcttactga	660
actatttgaa	cacatactag	aaaatatgga	ttcagttcat	ggaagacttg	tggatgagac	720
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gcaaaggcag	atgaagcagc	agcttgaggc	acttgcagac	ttacaacaaa	gcttgtgctc	900
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gcttttgctca	gccttaaagt	gaatcttaga	gctttctctt	gcttctgcta	ctcctacaga	1140
tggcctcatc	atggtctcca	ctcagtatta	ataactccat	cagcatagag	caaactcaac	1200
actgtgcatt	gcacactgtt	accatgggtt	tatgctcact	atcatatcac	attgcccaata	1260
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&lt;210&gt; 31

&lt;211&gt; 1355

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 31

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ctattttgaa	cagtggtagt	gtcctggatt	acttttcaga	aagaagtaat	cctttttatg	120
acagaacatg	taataatgaa	gtgggtcaaaa	tgcagaggct	aacattagaa	cacttgaatc	180
agatgggttg	aatcgagtac	atccttttgc	atgctcaaga	gccattctt	ttcatcattc	240
ggaagcaaca	gcggcagtc	cctgcccagg	ttatcccact	agctgattac	tatatcattg	300
ctggagtgat	ctatcaggca	ccagacttgg	gatcagttat	aaactctaga	gtgcttactg	360
cagtgcattg	tattcagtea	gctttttagt	aagctatgtc	atactgtcga	tatcatcctt	420
ccaaagggtg	ttgggtggac	ttcaaagatc	atgaagagca	agataaagtc	agacctaaag	480
ccaaaaggaa	agaagaacca	agctctatct	ttcagagaca	acgtgtggat	gctttacttt	540
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ttccagtggg	tcaaacaag	aaagaggcag	aacctatacc	agaaactgta	aaacctgagg	660
agaaggagac	cacaaagaat	gtacaacaga	cagtgagtgc	taaaggcccc	cctgaaaaac	720
ggatgagact	tcagtgagta	ctggacaaaa	gagaagcctg	gaagactcct	catgctagtt	780
atcatacctc	agtactgtgg	ctcttgagct	ttgaagtact	ttattgtaac	cttcttattt	840
gstatggaatg	cgcttatctt	ttgaaaggat	attaggccgg	atgtgggtgg	tcacgcctgt	900
aatcccagca	ctttgggagg	ccatggcggg	tggatcactt	gaggtcagaa	gttcaagacc	960
agcctgacca	atatggtgaa	accccgctct	tactaaaaat	acaaaaatta	gccggggcgtg	1020
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cgggaggtgg	aggttgccct	gagctgatta	tcattgctgt	gcactccagc	ttgggcgaca	1140
gaacgagact	ttgtctcaaa	aaaagaagaa	aagatattat	tcccatcatg	atttcttgtg	1200
aatatctgtt	atatgtcttc	tggtaacctt	tcctctcccc	gacttgaagc	aacctcacac	1260

actcacatgt ttactggttag atatgtttta aaagcaaaat aaagggtattt gtttttccaa 1320  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaac tcgag 1355

<210> 32  
 <211> 80  
 <212> PRT  
 <213> Homo sapien

<400> 32  
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 Thr Thr Pro Lys Lys Asp Lys His Gln Arg Lys Lys Val Gln Pro Ala  
 20 25 30  
 Val Leu Lys Tyr Tyr Lys Val Asp Glu Asn Gly Lys Ile Ser Cys Leu  
 35 40 45  
 Arg Arg Glu Cys Pro Ser Asp Glu Cys Gly Ala Gly Val Phe Met Ala  
 50 55 60  
 Ser His Phe Asp Arg His Tyr Cys Gly Lys Cys Cys Leu Thr His Cys  
 65 70 75 80

<210> 33  
 <211> 130  
 <212> PRT  
 <213> Homo sapien

<400> 33  
 Glu Ile Ser Asn Glu Val Arg Lys Phe Arg Thr Leu Thr Glu Leu Ile  
 1 5 10 15  
 Leu Asp Ala Gln Glu His Val Lys Asn Pro Tyr Lys Gly Lys Lys Leu  
 20 25 30  
 Lys Lys His Pro Asp Phe Pro Lys Lys Pro Leu Thr Pro Tyr Phe Arg  
 35 40 45  
 Phe Phe Met Glu Lys Arg Ala Lys Tyr Ala Lys Leu His Pro Gln Met  
 50 55 60  
 Ser Asn Leu Asp Leu Thr Lys Ile Leu Ser Lys Lys Tyr Lys Glu Leu  
 65 70 75 80  
 Pro Glu Lys Lys Lys Met Lys Tyr Val Pro Asp Phe Gln Arg Arg Glu  
 85 90 95  
 Thr Gly Val Arg Ala Lys Pro Gly Pro Ile Gln Gly Gly Ser Pro Pro  
 100 105 110  
 Pro Tyr Pro Glu Cys Gln Glu Ser Asp Ile Pro Glu Lys Pro Gln Asp  
 115 120 125  
 Pro Pro  
 130

<210> 34  
 <211> 506  
 <212> PRT  
 <213> Homo sapien

<400> 34  
 Asn Ser Glu Lys Glu Ile Pro Val Leu Asn Glu Leu Pro Val Pro Met  
 1 5 10 15  
 Val Ala Arg Tyr Ile Arg Ile Asn Pro Gln Ser Trp Phe Asp Asn Gly  
 20 25 30



Ser	Ile	Cys	Met	Arg	Met	Glu	Ile	Leu	Gly	Cys	Pro	Leu	Pro	Asp	Pro
		35					40					45			
Asn	Asn	Tyr	Tyr	His	Arg	Arg	Asn	Glu	Met	Thr	Thr	Thr	Asp	Asp	Leu
	50					55					60				
Asp	Phe	Lys	His	His	Asn	Tyr	Lys	Glu	Met	Arg	Gln	Leu	Met	Lys	Val
65					70					75					80
Val	Asn	Glu	Met	Cys	Pro	Asn	Ile	Thr	Arg	Ile	Tyr	Asn	Ile	Gly	Lys
				85					90					95	
Ser	His	Gln	Gly	Leu	Lys	Leu	Tyr	Ala	Val	Glu	Ile	Ser	Asp	His	Pro
			100					105					110		
Gly	Glu	His	Glu	Val	Gly	Glu	Pro	Glu	Phe	His	Tyr	Ile	Ala	Gly	Ala
		115					120						125		
His	Gly	Asn	Glu	Val	Leu	Gly	Arg	Glu	Leu	Leu	Leu	Leu	Leu	Leu	His
	130					135					140				
Phe	Leu	Cys	Gln	Glu	Tyr	Ser	Ala	Gln	Asn	Ala	Arg	Ile	Val	Arg	Leu
145					150					155					160
Val	Glu	Glu	Thr	Arg	Ile	His	Ile	Leu	Pro	Ser	Leu	Asn	Pro	Asp	Gly
				165					170					175	
Tyr	Glu	Lys	Ala	Tyr	Glu	Gly	Gly	Ser	Glu	Leu	Gly	Gly	Trp	Ser	Leu
			180				185						190		
Gly	Arg	Trp	Thr	His	Asp	Gly	Ile	Asp	Ile	Asn	Asn	Asn	Phe	Pro	Asp
	195					200						205			
Leu	Asn	Ser	Leu	Leu	Trp	Glu	Ala	Glu	Asp	Gln	Gln	Asn	Ala	Pro	Arg
	210					215					220				
Lys	Val	Pro	Asn	His	Tyr	Ile	Ala	Ile	Pro	Glu	Trp	Phe	Leu	Ser	Glu
225					230					235					240
Asn	Ala	Thr	Val	Ala	Thr	Glu	Thr	Arg	Ala	Val	Ile	Ala	Trp	Met	Glu
				245					250					255	
Lys	Ile	Pro	Phe	Val	Leu	Gly	Gly	Asn	Leu	Gln	Gly	Gly	Glu	Leu	Val
			260				265						270		
Val	Ala	Tyr	Pro	Tyr	Asp	Met	Val	Arg	Ser	Leu	Trp	Lys	Thr	Gln	Glu
		275					280					285			
His	Thr	Pro	Thr	Pro	Asp	Asp	His	Val	Phe	Arg	Trp	Leu	Ala	Tyr	Ser
	290				295						300				
Tyr	Ala	Ser	Thr	His	Arg	Leu	Met	Thr	Asp	Ala	Arg	Arg	Arg	Val	Cys
305					310					315					320
His	Thr	Glu	Asp	Phe	Gln	Lys	Glu	Glu	Gly	Thr	Val	Asn	Gly	Ala	Ser
				325					330					335	
Trp	His	Thr	Val	Ala	Gly	Ser	Leu	Asn	Asp	Phe	Ser	Tyr	Leu	His	Thr
			340					345					350		
Asn	Cys	Phe	Glu	Leu	Ser	Ile	Tyr	Val	Gly	Cys	Asp	Lys	Tyr	Pro	His
		355					360					365			
Glu	Ser	Glu	Leu	Pro	Glu	Glu	Trp	Glu	Asn	Asn	Arg	Glu	Ser	Leu	Ile
	370					375					380				
Val	Phe	Met	Glu	Gln	Val	His	Arg	Gly	Ile	Lys	Gly	Ile	Val	Arg	Asp
385					390					395					400
Leu	Gln	Gly	Lys	Gly	Ile	Ser	Asn	Ala	Val	Ile	Ser	Val	Glu	Gly	Val
				405					410					415	
Asn	His	Asp	Ile	Arg	Thr	Ala	Ser	Asp	Gly	Asp	Tyr	Trp	Arg	Leu	Leu
			420					425					430		
Asn	Pro	Gly	Glu	Tyr	Val	Val	Thr	Ala	Lys	Ala	Glu	Gly	Phe	Ile	Thr
		435					440					445			
Ser	Thr	Lys	Asn	Cys	Met	Val	Gly	Tyr	Asp	Met	Gly	Ala	Thr	Arg	Cys
450					455						460				
Asp	Phe	Thr	Leu	Thr	Lys	Thr	Asn	Leu	Ala	Arg	Ile	Arg	Glu	Ile	Met



465					470					475					480
Glu	Thr	Phe	Gly	Lys	Gln	Pro	Val	Ser	Leu	Pro	Ser	Arg	Arg	Leu	Lys
				485					490					495	
Leu	Arg	Gly	Arg	Lys	Arg	Arg	Gln	Arg	Gly						
			500					505							

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<210> 35
<211> 96
<212> PRT
<213> Homo sapien
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<div>&lt;400&gt; 35</div>															
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1				5					10					15	
Arg	Gly	Gln	Asp	Arg	Trp	Ser	Gln	Glu	Asp	Met	Leu	Thr	Leu	Leu	Glu
			20					25					30		
Cys	Met	Lys	Asn	Asn	Leu	Pro	Ser	Asn	Asp	Ser	Ser	Gln	Phe	Lys	Thr
		35					40					45			
Thr	Gln	Thr	His	Met	Asp	Arg	Glu	Lys	Val	Ala	Leu	Lys	Asp	Phe	Ser
	50					55					60				
Gly	Asp	Met	Cys	Lys	Leu	Lys	Trp	Val	Glu	Ile	Ser	Asn	Glu	Val	Arg
65					70					75					80
Lys	Phe	Arg	Thr	Leu	Thr	Glu	Leu	Ile	Leu	Asp	Thr	Gln	Glu	His	Val
				85					90					95	

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<210> 36
<211> 129
<212> PRT
<213> Homo sapien
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[illegible]

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<210> 37
<211> 238
<212> PRT
<213> Homo sapien
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&lt;400&gt; 37

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Asn	Ser	Gly	Ser	Val	Leu	Asp	Tyr	Phe	Ser	Glu	Arg	Ser	Asn	Pro	Phe
			20					25					30		
Tyr	Asp	Arg	Thr	Cys	Asn	Asn	Glu	Val	Val	Lys	Met	Gln	Arg	Leu	Thr
		35					40					45			
Leu	Glu	His	Leu	Asn	Gln	Met	Val	Gly	Ile	Glu	Tyr	Ile	Leu	Leu	His
	50					55					60				
Ala	Gln	Glu	Pro	Ile	Leu	Phe	Ile	Ile	Arg	Lys	Gln	Gln	Arg	Gln	Ser
65					70					75					80
Pro	Ala	Gln	Val	Ile	Pro	Leu	Ala	Asp	Tyr	Tyr	Ile	Ile	Ala	Gly	Val
				85					90					95	
Ile	Tyr	Gln	Ala	Pro	Asp	Leu	Gly	Ser	Val	Ile	Asn	Ser	Arg	Val	Leu
			100					105						110	
Thr	Ala	Val	His	Gly	Ile	Gln	Ser	Ala	Phe	Asp	Glu	Ala	Met	Ser	Tyr
		115					120					125			
Cys	Arg	Tyr	His	Pro	Ser	Lys	Gly	Tyr	Trp	Trp	His	Phe	Lys	Asp	His
	130					135					140				
Glu	Glu	Gln	Asp	Lys	Val	Arg	Pro	Lys	Ala	Lys	Arg	Lys	Glu	Glu	Pro
145					150					155					160
Ser	Ser	Ile	Phe	Gln	Arg	Gln	Arg	Val	Asp	Ala	Leu	Leu	Leu	Asp	Leu
				165					170					175	
Arg	Gln	Lys	Phe	Pro	Pro	Lys	Phe	Val	Gln	Leu	Lys	Pro	Gly	Glu	Lys
			180					185						190	
Pro	Val	Pro	Val	Asp	Gln	Thr	Lys	Lys	Glu	Ala	Glu	Pro	Ile	Pro	Glu
		195					200					205			
Thr	Val	Lys	Pro	Glu	Glu	Lys	Glu	Thr	Thr	Lys	Asn	Val	Gln	Gln	Thr
	210					215					220				
Val	Ser	Ala	Lys	Gly	Pro	Pro	Glu	Lys	Arg	Met	Arg	Leu	Gln		
225					230					235					

&lt;210&gt; 38

&lt;211&gt; 202

&lt;212&gt; PRT

&lt;213&gt; Homo sapien

&lt;400&gt; 38

Lys	Gly	Ser	Glu	Gly	Glu	Asn	Pro	Leu	Thr	Val	Pro	Gly	Arg	Glu	Lys
1				5					10					15	
Glu	Gly	Met	Leu	Met	Gly	Val	Lys	Pro	Gly	Glu	Asp	Ala	Ser	Gly	Pro
			20					25					30		
Ala	Glu	Asp	Leu	Val	Arg	Arg	Ser	Glu	Lys	Asp	Thr	Ala	Ala	Val	Val
		35					40					45			
Ser	Arg	Gln	Gly	Ser	Ser	Leu	Asn	Leu	Phe	Glu	Asp	Val	Gln	Ile	Thr
	50					55					60				
Glu	Pro	Glu	Ala	Glu	Pro	Glu	Ser	Lys	Ser	Glu	Pro	Arg	Pro	Pro	Ile
65					70					75					80
Ser	Ser	Pro	Arg	Ala	Pro	Gln	Thr	Arg	Ala	Val	Lys	Pro	Arg	Leu	His
				85					90					95	
Pro	Val	Lys	Pro	Met	Asn	Ala	Thr	Ala	Thr	Lys	Val	Ala	Asn	Cys	Ser
			100					105						110	
Leu	Gly	Thr	Ala	Thr	Ile	Ile	Gly	Glu	Asn	Leu	Asn	Asn	Glu	Val	Met
		115					120					125			
Met	Lys	Lys	Tyr	Ser	Pro	Ser	Asp	Pro	Ala	Phe	Ala	Tyr	Ala	Gln	Leu

130		135		140
Thr His Asp Glu Leu Ile	Gln Leu Val Leu Lys	Gln Lys Glu Thr Ile		
145		150	155	160
Ser Lys Lys Glu Phe Gln	Val Arg Glu Leu Glu	Asp Tyr Ile Asp Asn		
	165		170	175
Leu Leu Val Arg Val Met	Glu Glu Thr Pro Asn	Ile Leu Arg Ile Pro		
	180	185	190	
Thr Gln Val Gly Lys Lys	Ala Gly Lys Met			
195	200			

<210> 39  
 <211> 243  
 <212> PRT  
 <213> Homo sapien

<400> 39	
Val Asn Ala Leu Gly Ile Met Ala Ala Val Asp Ile Arg Asp Asn Leu	
1	5 10 15
Leu Gly Ile Ser Trp Val Asp Ser Ser Trp Ile Pro Ile Leu Asn Ser	
	20 25 30
Gly Ser Val Leu Asp Tyr Phe Ser Glu Arg Ser Asn Pro Phe Tyr Asp	
	35 40 45
Arg Thr Cys Asn Asn Glu Val Val Lys Met Gln Arg Leu Thr Leu Glu	
	50 55 60
His Leu Asn Gln Met Val Gly Ile Glu Tyr Ile Leu Leu His Ala Gln	
65	70 75 80
Glu Pro Ile Leu Phe Ile Ile Arg Lys Gln Gln Arg Gln Ser Pro Ala	
	85 90 95
Gln Val Ile Pro Leu Ala Asp Tyr Tyr Ile Ile Ala Gly Val Ile Tyr	
	100 105 110
Gln Ala Pro Asp Leu Gly Ser Val Ile Asn Ser Arg Val Leu Thr Ala	
	115 120 125
Val His Gly Ile Gln Ser Ala Phe Asp Glu Ala Met Ser Tyr Cys Arg	
	130 135 140
Tyr His Pro Ser Lys Gly Tyr Trp Trp His Phe Lys Asp His Glu Glu	
145	150 155 160
Gln Asp Lys Val Arg Pro Lys Ala Lys Arg Lys Glu Glu Pro Ser Ser	
	165 170 175
Ile Phe Gln Arg Gln Arg Val Asp Ala Leu Leu Leu Asp Leu Arg Gln	
	180 185 190
Lys Ile Ser Thr Gln Ile Cys Ala Val Asp Gln Thr Lys Lys Glu Ala	
	195 200 205
Glu Pro Ile Pro Glu Thr Val Lys Pro Glu Glu Lys Glu Thr Thr Lys	
	210 215 220
Asn Val Gln Gln Thr Val Ser Ala Lys Gly Pro Pro Glu Lys Arg Met	
225	230 235 240
Arg Leu Gln	

<210> 40  
 <211> 245  
 <212> PRT  
 <213> Homo sapien

<400> 40

Ala	Ala	Val	Asp	Ile	Arg	Asp	Asn	Leu	Leu	Gly	Ile	Ser	Trp	Val	Asp
1				5					10					15	
Ser	Ser	Trp	Ile	Pro	Ile	Leu	Asn	Ser	Gly	Ser	Val	Leu	Asp	Tyr	Phe
			20				25						30		
Ser	Glu	Arg	Ser	Asn	Pro	Phe	Tyr	Asp	Arg	Thr	Cys	Asn	Asn	Glu	Val
		35					40					45			
Val	Lys	Met	Gln	Arg	Leu	Thr	Leu	Glu	His	Leu	Asn	Gln	Met	Val	Gly
	50					55					60				
Ile	Glu	Tyr	Ile	Leu	Leu	His	Ala	Gln	Glu	Pro	Ile	Leu	Phe	Ile	Ile
65					70					75					80
Arg	Lys	Gln	Gln	Arg	Gln	Ser	Pro	Ala	Gln	Val	Ile	Pro	Leu	Ala	Asp
				85					90					95	
Tyr	Tyr	Ile	Ile	Ala	Gly	Val	Ile	Tyr	Gln	Ala	Pro	Asp	Leu	Gly	Ser
			100					105					110		
Val	Ile	Asn	Ser	Arg	Val	Leu	Thr	Ala	Val	His	Gly	Ile	Gln	Ser	Ala
		115					120					125			
Phe	Asp	Glu	Ala	Met	Ser	Tyr	Cys	Arg	Tyr	His	Pro	Ser	Lys	Gly	Tyr
	130					135					140				
Trp	Trp	His	Phe	Lys	Asp	His	Glu	Glu	Gln	Asp	Lys	Val	Arg	Pro	Lys
145					150					155					160
Ala	Lys	Arg	Lys	Glu	Glu	Pro	Ser	Ser	Ile	Phe	Gln	Arg	Gln	Arg	Val
				165					170					175	
Asp	Ala	Leu	Leu	Leu	Asp	Leu	Arg	Gln	Lys	Phe	Pro	Pro	Lys	Phe	Val
			180					185					190		
Gln	Leu	Lys	Pro	Gly	Glu	Lys	Pro	Val	Pro	Val	Asp	Gln	Thr	Lys	Lys
		195					200					205			
Glu	Ala	Glu	Pro	Ile	Pro	Glu	Thr	Val	Lys	Pro	Glu	Glu	Lys	Glu	Thr
	210					215					220				
Thr	Lys	Asn	Val	Gln	Gln	Thr	Val	Ser	Ala	Lys	Gly	Pro	Pro	Glu	Lys
225					230					235					240
Arg	Met	Arg	Leu	Gln											
				245											

<210> 41  
 <211> 163  
 <212> PRT  
 <213> Homo sapien

Gly	Glu	Arg	Gln	Gly	Leu	Val	Ala	Arg	Ala	Arg	Leu	Ser	Leu	Arg	Pro
1				5					10					15	
Ser	Ile	Pro	Glu	Leu	Ser	Glu	Arg	Thr	Ser	Arg	Pro	Cys	Arg	Ala	Ser
			20					25					30		
Pro	Ala	Ser	Leu	Pro	Ser	Gln	His	Thr	Ser	Ser	Pro	Ala	Gln	Ala	Arg
		35					40					45			
Val	Arg	Asn	Leu	Ala	Gln	Ser	Thr	Phe	Pro	Leu	Ala	Ala	Gln	Glu	Thr
	50					55					60				
Pro	Gly	Arg	Ala	Pro	Ala	His	Ala	Pro	Leu	Ser	Ser	Phe	Val	Pro	Gly
65					70					75					80
Val	Gly	Gly	Arg	Ser	Pro	Ala	Ser	Val	Gly	Ile	Ser	Ala	Pro	Gly	Gly
			85					90						95	
Gly	Pro	Ser	Gly	Ala	Ala	Ala	Lys	Ile	Pro	Leu	Glu	Leu	Thr	Gln	Ser
			100					105					110		
Arg	Val	Gln	Lys	Ile	Trp	Val	Pro	Val	Asp	His	Arg	Pro	Ser	Leu	Pro
		115					120					125			

20

Arg Ser Cys Gly Pro Lys Leu Thr Asn Ser Pro Ala Val Phe Val Met  
 130 135 140  
 Val Gly Leu Pro Arg Pro Gly Gln Asp Leu Leu Leu His Glu Ser Leu  
 145 150 155 160  
 Leu Ala Ala

<210> 42  
 <211> 243  
 <212> PRT  
 <213> Homo sapien

<400> 42  
 Val Asp Ile Arg Asp Asn Leu Leu Gly Ile Ser Trp Val Asp Ser Ser  
 1 5 10 15  
 Trp Ile Pro Ile Leu Asn Ser Gly Ser Val Leu Asp Tyr Phe Ser Glu  
 20 25 30  
 Arg Ser Asn Pro Phe Tyr Asp Arg Thr Cys Asn Asn Glu Val Val Lys  
 35 40 45  
 Met Gln Arg Leu Thr Leu Glu His Leu Asn Gln Met Val Gly Ile Glu  
 50 55 60  
 Tyr Ile Leu Leu His Ala Gln Glu Pro Ile Leu Phe Ile Ile Arg Lys  
 65 70 75 80  
 Gln Gln Arg Gln Ser Pro Ala Gln Val Ile Pro Leu Ala Asp Tyr Tyr  
 85 90 95  
 Ile Ile Ala Gly Val Ile Tyr Gln Ala Pro Asp Leu Gly Ser Val Ile  
 100 105 110  
 Asn Ser Arg Val Leu Thr Ala Val His Gly Ile Gln Ser Ala Phe Asp  
 115 120 125  
 Glu Ala Met Ser Tyr Cys Arg Tyr His Pro Ser Lys Gly Tyr Trp Trp  
 130 135 140  
 His Phe Lys Asp His Glu Glu Gln Asp Lys Val Arg Pro Lys Ala Lys  
 145 150 155 160  
 Arg Lys Glu Glu Pro Ser Ser Ile Phe Gln Arg Gln Arg Val Asp Ala  
 165 170 175  
 Leu Leu Leu Asp Leu Arg Gln Lys Phe Pro Pro Lys Phe Val Gln Leu  
 180 185 190  
 Lys Pro Gly Glu Lys Pro Val Pro Val Asp Gln Thr Lys Lys Glu Ala  
 195 200 205  
 Glu Pro Ile Pro Glu Thr Val Lys Pro Glu Glu Lys Glu Thr Thr Lys  
 210 215 220  
 Asn Val Gln Gln Thr Val Ser Ala Lys Gly Pro Pro Glu Lys Arg Met  
 225 230 235 240  
 Arg Leu Gln

<210> 43  
 <211> 244  
 <212> PRT  
 <213> Homo sapien

<400> 43  
 Ala Val Asp Ile Arg Asp Asn Leu Leu Gly Ile Ser Trp Val Asp Ser  
 1 5 10 15  
 Ser Trp Ile Pro Ile Leu Asn Ser Gly Ser Val Leu Asp Tyr Phe Ser

21

			20					25				30					
Glu	Arg	Ser	Asn	Pro	Phe	Tyr	Asp	Arg	Thr	Cys	Asn	Asn	Glu	Val	Val		
		35					40					45					
Lys	Met	Gln	Arg	Leu	Thr	Leu	Glu	His	Leu	Asn	Gln	Met	Val	Gly	Ile		
	50					55					60						
Glu	Tyr	Ile	Leu	Leu	His	Ala	Gln	Glu	Pro	Ile	Leu	Phe	Ile	Ile	Arg		
65					70					75					80		
Lys	Gln	Gln	Arg	Gln	Ser	Pro	Ala	Gln	Val	Ile	Pro	Leu	Ala	Asp	Tyr		
			85						90					95			
Tyr	Ile	Ile	Ala	Gly	Val	Ile	Tyr	Gln	Ala	Pro	Asp	Leu	Gly	Ser	Val		
			100					105					110				
Ile	Asn	Ser	Arg	Val	Leu	Thr	Ala	Val	His	Gly	Ile	Gln	Ser	Ala	Phe		
	115						120					125					
Asp	Glu	Ala	Met	Ser	Tyr	Cys	Arg	Tyr	His	Pro	Ser	Lys	Gly	Tyr	Trp		
	130					135					140						
Trp	His	Phe	Lys	Asp	His	Glu	Glu	Gln	Asp	Lys	Val	Arg	Pro	Lys	Ala		
145				150						155					160		
Lys	Arg	Lys	Glu	Glu	Pro	Ser	Ser	Ile	Phe	Gln	Arg	Gln	Arg	Val	Asp		
			165						170					175			
Ala	Leu	Leu	Leu	Asp	Leu	Arg	Gln	Lys	Phe	Pro	Pro	Lys	Phe	Val	Gln		
			180					185					190				
Leu	Lys	Pro	Gly	Glu	Lys	Pro	Val	Pro	Val	Asp	Gln	Thr	Lys	Lys	Glu		
	195						200					205					
Ala	Glu	Pro	Ile	Pro	Glu	Thr	Val	Lys	Pro	Glu	Glu	Lys	Glu	Thr	Thr		
	210					215					220						
Lys	Asn	Val	Gln	Gln	Thr	Val	Ser	Ala	Lys	Gly	Pro	Pro	Glu	Lys	Arg		
225					230					235					240		
Met	Arg	Leu	Gln														

&lt;210&gt; 44

&lt;211&gt; 109

&lt;212&gt; PRT

&lt;213&gt; Homo sapien

&lt;400&gt; 44

Glu	Leu	His	Phe	Ser	Glu	Phe	Thr	Ser	Ala	Val	Ala	Asp	Met	Lys	Asn		
1				5					10					15			
Ser	Val	Ala	Asp	Arg	Asp	Asn	Ser	Pro	Ser	Ser	Cys	Ala	Gly	Leu	Phe		
			20					25					30				
Ile	Ala	Ser	His	Ile	Gly	Phe	Asp	Trp	Pro	Gly	Val	Trp	Val	His	Leu		
	35					40						45					
Asp	Ile	Ala	Ala	Pro	Val	His	Ala	Gly	Glu	Arg	Ala	Thr	Gly	Phe	Gly		
	50					55					60						
Val	Ala	Leu	Leu	Leu	Ala	Leu	Phe	Gly	Arg	Ala	Ser	Glu	Asp	Pro	Leu		
65				70						75					80		
Leu	Asn	Leu	Val	Ser	Pro	Leu	Asp	Cys	Glu	Val	Asp	Ala	Gln	Glu	Gly		
			85					90					95				
Asp	Asn	Met	Gly	Arg	Asp	Ser	Lys	Arg	Arg	Arg	Leu	Val					
			100					105									

&lt;210&gt; 45

&lt;211&gt; 324

&lt;212&gt; PRT

&lt;213&gt; Homo sapien



<400> 45  
 Arg Arg Pro Val Met Ala Gln Glu Thr Ala Pro Pro Cys Gly Pro Val  
 1 5 10 15  
 Ser Arg Gly Asp Ser Pro Ile Ile Glu Lys Met Glu Lys Arg Thr Cys  
 20 25 30  
 Ala Leu Cys Pro Glu Gly His Glu Trp Ser Gln Ile Tyr Phe Ser Pro  
 35 40 45  
 Ser Gly Asn Ile Val Ala His Glu Asn Cys Leu Leu Tyr Ser Ser Gly  
 50 55 60  
 Leu Val Glu Cys Glu Thr Leu Asp Leu Arg Asn Thr Ile Arg Asn Phe  
 65 70 75 80  
 Asp Val Lys Ser Val Lys Lys Glu Ile Trp Arg Gly Arg Arg Leu Lys  
 85 90 95  
 Cys Ser Phe Cys Asn Lys Gly Gly Ala Thr Val Gly Cys Asp Leu Trp  
 100 105 110  
 Phe Cys Lys Lys Ser Tyr His Tyr Val Cys Ala Lys Lys Asp Gln Ala  
 115 120 125  
 Ile Leu Gln Val Asp Gly Asn His Gly Thr Tyr Lys Leu Phe Cys Pro  
 130 135 140  
 Glu His Ser Pro Glu Gln Glu Glu Ala Thr Glu Ser Ala Asp Asp Pro  
 145 150 155 160  
 Ser Met Lys Lys Lys Arg Gly Lys Asn Lys Arg Leu Ser Ser Gly Pro  
 165 170 175  
 Pro Ala Gln Pro Lys Thr Met Lys Cys Ser Asn Ala Lys Arg His Met  
 180 185 190  
 Thr Glu Glu Pro His Gly His Thr Asp Ala Ala Val Lys Ser Pro Phe  
 195 200 205  
 Leu Lys Lys Cys Gln Glu Ala Gly Leu Leu Thr Glu Leu Phe Glu His  
 210 215 220  
 Ile Leu Glu Asn Met Asp Ser Val His Gly Arg Leu Val Asp Glu Thr  
 225 230 235 240  
 Ala Ser Glu Ser Asp Tyr Glu Gly Ile Glu Thr Leu Leu Phe Asp Cys  
 245 250 255  
 Gly Leu Phe Lys Asp Thr Leu Arg Lys Phe Gln Glu Val Ile Lys Ser  
 260 265 270  
 Lys Ala Cys Glu Trp Glu Glu Arg Gln Arg Gln Met Lys Gln Gln Leu  
 275 280 285  
 Glu Ala Leu Ala Asp Leu Gln Gln Ser Leu Cys Ser Phe Gln Glu Asn  
 290 295 300  
 Gly Asp Leu Asp Cys Ser Ser Ser Thr Ser Gly Ser Leu Leu Pro Pro  
 305 310 315 320  
 Glu Asp His Gln

&lt;210&gt; 46

&lt;211&gt; 244

&lt;212&gt; PRT

&lt;213&gt; Homo sapien

&lt;400&gt; 46

Ala Val Asp Ile Arg Asp Asn Leu Leu Gly Ile Ser Trp Val Asp Ser  
 1 5 10 15  
 Ser Trp Ile Pro Ile Leu Asn Ser Gly Ser Val Leu Asp Tyr Phe Ser  
 20 25 30

23

Glu Arg Ser Asn Pro Phe Tyr Asp Arg Thr Cys Asn Asn Glu Val Val  
           35                          40                          45  
 Lys Met Gln Arg Leu Thr Leu Glu His Leu Asn Gln Met Val Gly Ile  
       50                          55                          60  
 Glu Tyr Ile Leu Leu His Ala Gln Glu Pro Ile Leu Phe Ile Ile Arg  
 65                          70                          75                          80  
 Lys Gln Gln Arg Gln Ser Pro Ala Gln Val Ile Pro Leu Ala Asp Tyr  
                           85                          90                          95  
 Tyr Ile Ile Ala Gly Val Ile Tyr Gln Ala Pro Asp Leu Gly Ser Val  
                          100                         105                         110  
 Ile Asn Ser Arg Val Leu Thr Ala Val His Gly Ile Gln Ser Ala Phe  
           115                         120                         125  
 Asp Glu Ala Met Ser Tyr Cys Arg Tyr His Pro Ser Lys Gly Tyr Trp  
       130                         135                         140  
 Trp His Phe Lys Asp His Glu Glu Gln Asp Lys Val Arg Pro Lys Ala  
 145                         150                         155                         160  
 Lys Arg Lys Glu Glu Pro Ser Ser Ile Phe Gln Arg Gln Arg Val Asp  
                          165                         170                         175  
 Ala Leu Leu Leu Asp Leu Arg Gln Lys Phe Pro Pro Lys Phe Val Gln  
                          180                         185                         190  
 Leu Lys Pro Gly Glu Lys Pro Val Pro Val Asp Gln Thr Lys Lys Glu  
           195                         200                         205  
 Ala Glu Pro Ile Pro Glu Thr Val Lys Pro Glu Glu Lys Glu Thr Thr  
       210                         215                         220  
 Lys Asn Val Gln Gln Thr Val Ser Ala Lys Gly Pro Pro Glu Lys Arg  
 225                         230                         235                         240  
 Met Arg Leu Gln

<210> 47  
 <211> 14  
 <212> DNA  
 <213> Homo sapien

<400> 47  
 tttttttttt ttag

14

<210> 48  
 <211> 10  
 <212> DNA  
 <213> Homo sapien

<400> 48  
 cttcaacctc

10

<210> 49  
 <211> 496  
 <212> DNA  
 <213> Homo sapien

<400> 49  
 gcaccatgta ccgagcactt cggctcctcg cgcgctcgcg tcccctcgtg cgggctccag 60  
 ccgcagcctt agcttcggct cccggcttgg gtggcgcggc cgtgccctcg ttttggcctc 120  
 cgaacgcggc tcgaatggca agccaaaatt ccttccggat agaatatgat acctttgggtg 180  
 aactaaaggt gccaaatgat aagtattatg gcgcccagac cgtgagatct acgatgaact 240

ttaagattgg	aggtgtgaca	gaacgcatgc	caacccccagt	tattaaagct	tttggcatct	300
tgaagcgagc	ggccgctgaa	gtaaaccagg	attatgggtct	tgatccaaag	attgctaattg	360
caataatgaa	ggcagcagat	gaggtagctg	aaggtaaatt	aaatgatcat	tttcctctcg	420
tggtatggca	gactggatca	ggaactcaga	caaatatgaa	tgtaaattgaa	gtcattagcc	480
aatagagcaa	ttgaaa					496

<210> 50  
 <211> 499  
 <212> DNA  
 <213> Homo sapien

<400> 50						
agaaaaagtc	tatgttttgca	gaaatacaga	tccaagacaa	agacaggatg	ggcactgctg	60
gaaaagttat	taaatgcaaa	gcagctgtgc	tttgggagca	gaagcaaccc	ttctccattg	120
aggaaataga	agttgccccca	ccaaagacta	aagaagttcg	cattaagatt	ttggccacag	180
gaatctgtcg	cacagatgac	catgtgataa	aaggaacaat	gggtgtccaag	tttccagtga	240
ttgtgggaca	tgaggcaact	gggattgtag	agagcattgg	agaaggagtg	actacagtga	300
aaccaggtga	caaagtcatt	cctctctttc	tgccacaatg	tagagaatgc	aatgcttgct	360
gcaacccaga	tggcaacctt	tgcattagga	gcgatattac	tggtcgtgga	gtactggctg	420
atggcaccac	cagattttaca	tgcaagggcg	aaccagtcca	ccacttcattg	aacaccagta	480
catttaccga	gtacacagt					499

<210> 51  
 <211> 887  
 <212> DNA  
 <213> Homo sapien

<400> 51						
gagtctgagc	agaaaggaaa	agcagccttg	gcagccacgt	tagaggaata	caaagccaca	60
gtggccagtg	accagataga	gatgaatcgc	ctgaaggctc	agctggagaa	tgaaaagcag	120
aaagtggcag	agctgtattc	tatccataac	tctggagaca	aatctgatat	tcaggacctc	180
ctggagagtg	tcaggctgga	caaagaaaaa	gcagagactt	tggctagtag	cttgcaggaa	240
gatctggctc	atacccgaaa	tgatgccaat	cgattacagg	atgccattgc	taaggtagag	300
gatgaatacc	gagccttcca	agaagaagct	aagaaacaaa	ttgaagattt	gaatatgacg	360
ttagaaaaat	taagatcaga	cctggatgaa	aaagaaacag	aaaggagtga	catgaaagaa	420
accatctttg	aacttgaaga	tgaagtagaa	caacatcggt	ctgtgaaact	tcatgacaac	480
ctcattattt	ctgatctaga	gaatacagtt	aaaaaactcc	aggaccaaaa	gcacgacatg	540
gaaagagaaa	taaagacact	ccacagaaga	cttcgggaag	aatctgcgga	atggcggcag	600
tttcaggctg	atctccagac	tgcatgtatc	attgcaaattg	acattaaatc	tgaagcccaa	660
gaggagattg	gtgatctaaa	gcgccgggta	catgaggctc	aagaaaaaaa	tgagaaactc	720
acaaaagaat	tggaggaaat	aaagtcacgc	aagcaagagg	aggagcagag	cgggtataca	780
attacatgaa	tgccgttgag	agagattttg	cagccttaag	gcagggaatg	ggactgagta	840
gaaggtcctc	gacttctca	gagccaactc	ctacagtaaa	aaccctc		887

<210> 52  
 <211> 491  
 <212> DNA  
 <213> Homo sapien

<400> 52						
ggcacgagct	tttccaaaaa	tcattgctgct	cctttctcta	aagttcttac	attttataga	60
aaggaaacctt	tcactcttga	ggcctactac	agctctcctc	aggatttgcc	ctatccagat	120
cctgctatag	ctcagttttc	agttcagaaa	gtcactcctc	agtctgatgg	ctccagttca	180
aaagtgaag	tcaaagttcg	agtaaattgtc	catggcattt	tcagtgtgtc	cagtgcattc	240
ttagtggagg	ttcacaagtc	tgaggaaaat	gaggagccaa	tggaaacaga	tcagaatgca	300

aaggaggaag	agaagatgca	agtggaccag	gaggaaccac	atgttgaaga	gcaacagcag	360
cagacaccag	gcagaaaata	aggcagagtc	tgaagaaatg	gagacctctc	aagctggatc	420
caaggataaa	aagatggacc	aaccacccca	agccaagaag	gcaaaagtga	agaccagtac	480
tgtggacctg	g					491

&lt;210&gt; 53

&lt;211&gt; 787

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 53

aagcagttga	gtaggcagaa	aaaagaacct	cttcattaag	gattaaaatg	tataggccag	60
cacgtgtaac	ttcgacttca	agattttctga	atccatatgt	agtatgtttc	attgtcgtcg	120
caggggtagt	gaccttgga	gtcaccatag	ctctacttgt	ttacttttta	gcttttgatc	180
aaaaatctta	cttttatagg	agcagttttc	aactcctaaa	tgttgaatat	aatagtcagt	240
taaattcacc	agctacacag	gaatacagga	ctttgagtgg	aagaattgaa	tctctgatta	300
ctaaaacatt	caaagaatca	aattttaagaa	atcagttcat	cagagctcat	gttgccaaac	360
tgaggcaaga	tggtagtgg	gtgagagcgg	atgttgatcat	gaaatttcaa	ttcactagaa	420
ataacaatgg	agcatcaatg	aaaagcagaa	ttgagtctgt	tttacgacaa	atgctgaata	480
actctggaaa	cctggaaata	aacccttcaa	ctgagataac	atcacttact	gaccaggctg	540
cagcaaattg	gcttattaat	gaatgtgggg	ccggtccaga	cctaataaca	ttgtctgagc	600
agagaatcct	tgagggcact	gaggctgagg	agggaagctg	gccgtggcaa	gtcagtcctgc	660
ggctcaataa	tgcccaccac	tgtggaggca	gcctgatcaa	taacatgtgg	atcctgacag	720
cagctcactg	cttcagaagc	aactctaate	ctcgtgactg	gattgccacg	tctgggtattt	780
ccacaac						787

&lt;210&gt; 54

&lt;211&gt; 386

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 54

ggcattttca	gtgtgtccag	tgcattcttta	gtggagggttc	acaagtctga	ggaaaatgag	60
gagccaatgg	aaacagatca	gaatgcaaag	gaggaagaga	agatgcaagt	ggaccaggag	120
gaaccacatg	ttgaagagca	acagcagcag	acaccagcag	aaaataaggc	agagtctgaa	180
gaaatggaga	cctctcaagc	tggatccaag	gataaaaaga	tggaccaacc	acccaagcc	240
aagaaggcaa	aagtgaagac	cagtactgtg	gacctgcaa	tcgagaatca	gctattatgg	300
cagatagaca	gagagatgct	caacttgtac	attgaaaatg	agggttaagat	gatcatgcag	360
gataaactgg	agaaggagcg	gaatga				386

&lt;210&gt; 55

&lt;211&gt; 1462

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 55

aagcagttga	gtaggcagaa	aaaagaacct	cttcattaag	gattaaaatg	tataggccag	60
cacgtgtaac	ttcgacttca	agattttctga	atccatatgt	agtatgtttc	attgtcgtcg	120
caggggtagt	gaccttgga	gtcaccatag	ctctacttgt	ttacttttta	gcttttgatc	180
aaaaatctta	cttttatagg	agcagttttc	aactcctaaa	tgttgaatat	aatagtcagt	240
taaattcacc	agctacacag	gaatacagga	ctttgagtgg	aagaattgaa	tctctgatta	300
ctaaaacatt	caaagaatca	aattttaagaa	atcagttcat	cagagctcat	gttgccaaac	360
tgaggcaaga	tggtagtgg	gtgagagcgg	atgttgatcat	gaaatttcaa	ttcactagaa	420
ataacaatgg	agcatcaatg	aaaagcagaa	ttgagtctgt	tttacgacaa	atgctgaata	480
actctggaaa	cctggaaata	aacccttcaa	ctgagataac	atcacttact	gaccaggctg	540

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cagcaaattg gcttattaat gaatgtgggg ccggtccaga cctaataaca ttgtctgagc      600
agagaatcct tggaggcact gaggtgagg agggagctg gccgtggcaa gtcagtctgc      660
ggctcaataa tgcccaccac tgtggaggca gcctgatcaa taacatgtgg atcctgacag      720
cagctcactg cttcagaagc aactctaate ctcgtgactg gattgccacg tctggtattt      780
ccacaacatt tcctaaacta agaatgagag taagaaatat tttaattcat aacaattata      840
aatctgcaac tcatgaaaat gacattgcac ttgtgagact tgagaacagt gtcaccttta      900
ccaaagatat ccatagtgtg tgtctcccag ctgctaccca gaatattcca cctggctcta      960
ctgcttatgt aacaggatgg ggcgctcaag aatatgctgg ccacacagtt ccagagctaa     1020
ggcaaggaca ggtcagaata ataagtaatg atgtatgtaa tgcaccacat agttataatg     1080
gagccatctt gtctggaatg ctgtgtgctg gagtacctca aggtggagtg gacgcatgtc     1140
agggtgactc tgggtggcca ctagtacaag aagactcacg gcggcttttg tttattgtgg     1200
ggatagtaag ctggggagat cagtgtggcc tgccggataa gccaggagtg tatactcgag     1260
tgacagcata cattgactgg attaggcaac aaactgggat ctagtgcaac aagtgcaccc     1320
ctgttgcaaa gtctgtatgc aggtgtgcct gtcttaaatt ccaaagcttt acatttcaac     1380
tgaaaaagaa actagaaatg tcctaattta acatcttggt acataaatat ggtttaacaa     1440
aaaaaaaaa aaaaaactcg ag                                           1462

```

<210> 56  
 <211> 159  
 <212> PRT  
 <213> Homo sapien

```

<400> 56
Thr Met Tyr Arg Ala Leu Arg Leu Leu Ala Arg Ser Arg Pro Leu Val
 1          5          10          15
Arg Ala Pro Ala Ala Ala Leu Ala Ser Ala Pro Gly Leu Gly Gly Ala
          20          25          30
Ala Val Pro Ser Phe Trp Pro Pro Asn Ala Ala Arg Met Ala Ser Gln
          35          40          45
Asn Ser Phe Arg Ile Glu Tyr Asp Thr Phe Gly Glu Leu Lys Val Pro
          50          55          60
Asn Asp Lys Tyr Tyr Gly Ala Gln Thr Val Arg Ser Thr Met Asn Phe
65          70          75          80
Lys Ile Gly Gly Val Thr Glu Arg Met Pro Thr Pro Val Ile Lys Ala
          85          90          95
Phe Gly Ile Leu Lys Arg Ala Ala Ala Glu Val Asn Gln Asp Tyr Gly
          100          105          110
Leu Asp Pro Lys Ile Ala Asn Ala Ile Met Lys Ala Ala Asp Glu Val
          115          120          125
Ala Glu Gly Lys Leu Asn Asp His Phe Pro Leu Val Val Trp Gln Thr
          130          135          140
Gly Ser Gly Thr Gln Thr Asn Met Asn Val Asn Glu Val Ile Ser
145          150          155

```

<210> 57  
 <211> 165  
 <212> PRT  
 <213> Homo sapien

```

<400> 57
Lys Lys Ser Met Phe Ala Glu Ile Gln Ile Gln Asp Lys Asp Arg Met
 1          5          10          15
Gly Thr Ala Gly Lys Val Ile Lys Cys Lys Ala Ala Val Leu Trp Glu
          20          25          30
Gln Lys Gln Pro Phe Ser Ile Glu Glu Ile Glu Val Ala Pro Pro Lys

```

```
<210> 58
<211> 259
<212> PRT
<213> Homo sapien
```

<div> <div>&lt;400&gt;</div> <div>58</div> </div>															
Glu 1	Ser	Glu	Gln	Lys	Gly	Lys	Ala	Ala	Leu	Ala	Ala	Thr	Leu	Glu	Glu
				5					10					15	
Tyr	Lys	Ala	Thr	Val	Ala	Ser	Asp	Gln	Ile	Glu	Met	Asn	Arg	Leu	Lys
			20					25					30		
Ala	Gln	Leu	Glu	Asn	Glu	Lys	Gln	Lys	Val	Ala	Glu	Leu	Tyr	Ser	Ile
		35					40					45			
His	Asn	Ser	Gly	Asp	Lys	Ser	Asp	Ile	Gln	Asp	Leu	Leu	Glu	Ser	Val
	50					55					60				
Arg 65	Leu	Asp	Lys	Glu	Lys	Ala	Glu	Thr	Leu	Ala	Ser	Ser	Leu	Gln	Glu
					70					75					80
Asp	Leu	Ala	His	Thr	Arg	Asn	Asp	Ala	Asn	Arg	Leu	Gln	Asp	Ala	Ile
			85						90					95	
Ala	Lys	Val	Glu	Asp	Glu	Tyr	Arg	Ala	Phe	Gln	Glu	Glu	Ala	Lys	Lys
			100					105					110		
Gln	Ile	Glu	Asp	Leu	Asn	Met	Thr	Leu	Glu	Lys	Leu	Arg	Ser	Asp	Leu
		115					120					125			
Asp	Glu	Lys	Glu	Thr	Glu	Arg	Ser	Asp	Met	Lys	Glu	Thr	Ile	Phe	Glu
	130					135					140				
Leu 145	Glu	Asp	Glu	Val	Glu	Gln	His	Arg	Ala	Val	Lys	Leu	His	Asp	Asn
					150					155					160
Leu	Ile	Ile	Ser	Asp	Leu	Glu	Asn	Thr	Val	Lys	Lys	Leu	Gln	Asp	Gln
			165						170					175	
Lys	His	Asp	Met	Glu	Arg	Glu	Ile	Lys	Thr	Leu	His	Arg	Arg	Leu	Arg
			180					185						190	
Glu	Glu	Ser	Ala	Glu	Trp	Arg	Gln	Phe	Gln	Ala	Asp	Leu	Gln	Thr	Ala
		195					200					205			
Val	Val	Ile	Ala	Asn	Asp	Ile	Lys	Ser	Glu	Ala	Gln	Glu	Glu	Ile	Gly
	210					215					220				
Asp 225	Leu	Lys	Arg	Arg	Leu	His	Glu	Ala	Gln	Glu	Lys	Asn	Glu	Lys	Leu
					230					235					240
Thr	Lys	Glu	Leu	Glu	Glu	Ile	Lys	Ser	Arg	Lys	Gln	Glu	Glu	Glu	Arg



28

245

250

255

Gly Gly Tyr

<210> 59  
 <211> 125  
 <212> PRT  
 <213> Homo sapien

&lt;400&gt; 59

Gly	Thr	Ser	Phe	Ser	Lys	Asn	His	Ala	Ala	Pro	Phe	Ser	Lys	Val	Leu
1				5					10					15	
Thr	Phe	Tyr	Arg	Lys	Glu	Pro	Phe	Thr	Leu	Glu	Ala	Tyr	Tyr	Ser	Ser
			20					25					30		
Pro	Gln	Asp	Leu	Pro	Tyr	Pro	Asp	Pro	Ala	Ile	Ala	Gln	Phe	Ser	Val
		35					40					45			
Gln	Lys	Val	Thr	Pro	Gln	Ser	Asp	Gly	Ser	Ser	Ser	Lys	Val	Lys	Val
	50					55					60				
Lys	Val	Arg	Val	Asn	Val	His	Gly	Ile	Phe	Ser	Val	Ser	Ser	Ala	Ser
65					70					75					80
Leu	Val	Glu	Val	His	Lys	Ser	Glu	Glu	Asn	Glu	Glu	Pro	Met	Glu	Thr
				85					90					95	
Asp	Gln	Asn	Ala	Lys	Glu	Glu	Glu	Lys	Met	Gln	Val	Asp	Gln	Glu	Glu
			100					105					110		
Pro	His	Val	Glu	Glu	Gln	Gln	Gln	Gln	Thr	Pro	Gly	Arg			
		115					120					125			

<210> 60  
 <211> 246  
 <212> PRT  
 <213> Homo sapien

&lt;400&gt; 60

Met	Tyr	Arg	Pro	Ala	Arg	Val	Thr	Ser	Thr	Ser	Arg	Phe	Leu	Asn	Pro
1				5					10					15	
Tyr	Val	Val	Cys	Phe	Ile	Val	Val	Ala	Gly	Val	Val	Ile	Leu	Ala	Val
			20					25					30		
Thr	Ile	Ala	Leu	Leu	Val	Tyr	Phe	Leu	Ala	Phe	Asp	Gln	Lys	Ser	Tyr
		35					40					45			
Phe	Tyr	Arg	Ser	Ser	Phe	Gln	Leu	Leu	Asn	Val	Glu	Tyr	Asn	Ser	Gln
	50					55					60				
Leu	Asn	Ser	Pro	Ala	Thr	Gln	Glu	Tyr	Arg	Thr	Leu	Ser	Gly	Arg	Ile
65					70					75					80
Glu	Ser	Leu	Ile	Thr	Lys	Thr	Phe	Lys	Glu	Ser	Asn	Leu	Arg	Asn	Gln
				85					90					95	
Phe	Ile	Arg	Ala	His	Val	Ala	Lys	Leu	Arg	Gln	Asp	Gly	Ser	Gly	Val
			100					105					110		
Arg	Ala	Asp	Val	Val	Met	Lys	Phe	Gln	Phe	Thr	Arg	Asn	Asn	Asn	Gly
		115					120					125			
Ala	Ser	Met	Lys	Ser	Arg	Ile	Glu	Ser	Val	Leu	Arg	Gln	Met	Leu	Asn
		130				135					140				
Asn	Ser	Gly	Asn	Leu	Glu	Ile	Asn	Pro	Ser	Thr	Glu	Ile	Thr	Ser	Leu
145					150					155					160
Thr	Asp	Gln	Ala	Ala	Ala	Asn	Trp	Leu	Ile	Asn	Glu	Cys	Gly	Ala	Gly
				165					170					175	

[illegible]

```
<210> 61
<211> 128
<212> PRT
<213> Homo sapien
```

<400> 61															
Gly	Ile	Phe	Ser	Val	Ser	Ser	Ala	Ser	Leu	Val	Glu	Val	His	Lys	Ser
1				5					10					15	
Glu	Glu	Asn	Glu	Glu	Pro	Met	Glu	Thr	Asp	Gln	Asn	Ala	Lys	Glu	Glu
			20					25					30		
Glu	Lys	Met	Gln	Val	Asp	Gln	Glu	Glu	Pro	His	Val	Glu	Glu	Gln	Gln
		35					40					45			
Gln	Gln	Thr	Pro	Ala	Glu	Asn	Lys	Ala	Glu	Ser	Glu	Glu	Met	Glu	Thr
	50					55					60				
Ser	Gln	Ala	Gly	Ser	Lys	Asp	Lys	Lys	Met	Asp	Gln	Pro	Pro	Gln	Ala
65					70					75					80
Lys	Lys	Ala	Lys	Val	Lys	Thr	Ser	Thr	Val	Asp	Leu	Pro	Ile	Glu	Asn
				85					90					95	
Gln	Leu	Leu	Trp	Gln	Ile	Asp	Arg	Glu	Met	Leu	Asn	Leu	Tyr	Ile	Glu
			100					105					110		
Asn	Glu	Gly	Lys	Met	Ile	Met	Gln	Asp	Lys	Leu	Glu	Lys	Glu	Arg	Asn
		115					120					125			

```
<210> 62
<211> 418
<212> PRT
<213> Homo sapien
```

Met															
Met Tyr Arg Pro Ala Arg Val Thr Ser Thr Ser Arg Phe Leu Asn Pro															
1				5					10					15	
Tyr	Val	Val	Cys	Phe	Ile	Val	Val	Ala	Gly	Val	Val	Ile	Leu	Ala	Val
			20					25					30		
Thr	Ile	Ala	Leu	Leu	Val	Tyr	Phe	Leu	Ala	Phe	Asp	Gln	Lys	Ser	Tyr
		35					40					45			
Phe	Tyr	Arg	Ser	Ser	Phe	Gln	Leu	Leu	Asn	Val	Glu	Tyr	Asn	Ser	Gln
	50					55					60				
Leu	Asn	Ser	Pro	Ala	Thr	Gln	Glu	Tyr	Arg	Thr	Leu	Ser	Gly	Arg	Ile
65					70					75					80
Glu	Ser	Leu	Ile	Thr	Lys	Thr	Phe	Lys	Glu	Ser	Asn	Leu	Arg	Asn	Gln
				85					90					95	
Phe	Ile	Arg	Ala	His	Val	Ala	Lys	Leu	Arg	Gln	Asp	Gly	Ser	Gly	Val
			100					105					110		
Arg	Ala	Asp	Val	Val	Met	Lys	Phe	Gln	Phe	Thr	Arg	Asn	Asn	Asn	Gly

115	120	125
Ala Ser Met Lys Ser Arg Ile Glu Ser Val Leu Arg Gln Met Leu Asn		
130	135	140
Asn Ser Gly Asn Leu Glu Ile Asn Pro Ser Thr Glu Ile Thr Ser Leu		
145	150	155
Thr Asp Gln Ala Ala Ala Asn Trp Leu Ile Asn Glu Cys Gly Ala Gly		160
	165	170
Pro Asp Leu Ile Thr Leu Ser Glu Gln Arg Ile Leu Gly Gly Thr Glu		175
	180	185
Ala Glu Glu Gly Ser Trp Pro Trp Gln Val Ser Leu Arg Leu Asn Asn		190
195	200	205
Ala His His Cys Gly Gly Ser Leu Ile Asn Asn Met Trp Ile Leu Thr		
210	215	220
Ala Ala His Cys Phe Arg Ser Asn Ser Asn Pro Arg Asp Trp Ile Ala		
225	230	235
Thr Ser Gly Ile Ser Thr Thr Phe Pro Lys Leu Arg Met Arg Val Arg		240
	245	250
Asn Ile Leu Ile His Asn Asn Tyr Lys Ser Ala Thr His Glu Asn Asp		255
	260	265
Ile Ala Leu Val Arg Leu Glu Asn Ser Val Thr Phe Thr Lys Asp Ile		270
275	280	285
His Ser Val Cys Leu Pro Ala Ala Thr Gln Asn Ile Pro Pro Gly Ser		
290	295	300
Thr Ala Tyr Val Thr Gly Trp Gly Ala Gln Glu Tyr Ala Gly His Thr		310
305	315	320
Val Pro Glu Leu Arg Gln Gly Gln Val Arg Ile Ile Ser Asn Asp Val		
	325	330
Cys Asn Ala Pro His Ser Tyr Asn Gly Ala Ile Leu Ser Gly Met Leu		335
	340	345
Cys Ala Gly Val Pro Gln Gly Gly Val Asp Ala Cys Gln Gly Asp Ser		350
355	360	365
Gly Gly Pro Leu Val Gln Glu Asp Ser Arg Arg Leu Trp Phe Ile Val		
370	375	380
Gly Ile Val Ser Trp Gly Asp Gln Cys Gly Leu Pro Asp Lys Pro Gly		
385	390	395
Val Tyr Thr Arg Val Thr Ala Tyr Ile Asp Trp Ile Arg Gln Gln Thr		400
	405	410
		415

Gly Ile

&lt;210&gt; 63

&lt;211&gt; 776

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 63

cacagatggt gatagaggaa tccatcttgc agtcagataa agccctcact gatagagaga	60
aggcagtagc agtggatcgg gccagaagg aggcagctga gaaggaacag gaacttttaa	120
aacagaaatt acaggagcag ccagcaacag atggaggctc aagataagag tcgcaaggaa	180
aactagccaa ctgaaggaga agctgcagat ggagagagaa cacctactga gagagcagat	240
tatgatgttg gagcacacgc agaaggtcca aaatgatttg cttcatgaag gatttaagaa	300
gaagtatgag gagatgaatg cagagataag tcaatttaaa cgtatgattg atactacaaa	360
aaatgatgat actccttgga ttgcacgaac cttggacaac cttgccgatg agctaactgc	420
aatattgtct gctcctgcta aattaattgg tcatggtgtc aaaggtgtga gctcactctt	480
taaaaagcat aagctcccct tttaaggata ttatagattg tacatatatg ctttggacta	540

tttttgatct gtatgttttt cattttcatt cagcaagttt tttttttttt tcagagtctt	600
actctgttgc ccaggctgga gtacagtggg gcaatctcag ctactgcaa cctctgcctc	660
ctgggttcaa gagattcacc tgcctcagcc ccctagtagc tgggattata ggtgtacacc	720
accacaccca gctaattttt gtatttttag tagagatggg gtttcactat gttggc	776

<210> 64  
 <211> 160  
 <212> DNA  
 <213> Homo sapien

<400> 64	
gcagcgtctt cggttgcaagt acccactgga aggacttagg cgctcgcgtg gacaccgcaa	60
gcccctcagt agcctcggcc caagaggcct gctttccact cgctagcccc gccggggggtc	120
cgtgtcctgt ctcgggtggcc ggaccggggc ccgagccccga	160

<210> 65  
 <211> 72  
 <212> PRT  
 <213> Homo sapien

<400> 65	
Leu Ser Ala Met Gly Phe Thr Ala Ala Gly Ile Ala Ser Ser Ser Ile	
1 5 10 15	
Ala Ala Lys Met Met Ser Ala Ala Ala Ile Ala Asn Gly Gly Gly Val	
20 25 30	
Ala Ser Gly Ser Leu Val Ala Thr Leu Gln Ser Leu Gly Ala Thr Gly	
35 40 45	
Leu Ser Gly Leu Thr Lys Phe Ile Leu Gly Ser Ile Gly Ser Ala Ile	
50 55 60	
Ala Ala Val Ile Ala Arg Phe Tyr	
65 70	

<210> 66  
 <211> 2581  
 <212> DNA  
 <213> Homo sapien

<400> 66	
ctttcaaccc gcgctcgccg gctccagccc cgcgcgcccc cacccttgc cctcccggcg	60
gctccgcagg gtgaggtggc tttgaccccg ggttgcccgg ccagcacgac cgaggagggtg	120
gctggacagc tggaggatga acggagaagc cgactgcccc acagacctgg aaatggccgc	180
cccaaaggc caagaccgtt ggtcccagga agacatgctg actttgctgg aatgcatgaa	240
gaacaacctt ccatccaatg acagctccaa gttcaaaacc accgaatcac acatggactg	300
ggaaaaagta gcatttaaag acttttctgg agacatgtgc aagctcaaat ggggtggagat	360
ttctaataag gtgaggaagt tccgtacatt gacagaattg atcctcgatg ctcaggaaca	420
tgttaaaaat ccttacaaag gcaaaaaact caagaaacac ccagacttcc caaagaagcc	480
cctgacccct tatttccgct tcttcatgga gaagcggggc aagtatgcga aactccaccc	540
tgagatgagc aacctggacc taaccaagat tctgtccaag aaatacaagg agcttccgga	600
gaagaagaag atgaaatata ttcaggactt ccagagagag aaacaggagt tcgagcgaaa	660
cctggcccga ttcaggaggg atcaccccga cctaattccag aatgccaaaga aatcggacat	720
cccagagaag cccaaaaccc cccagcagct gtggtacacc cacgagaaga aggtgtatct	780
caaagtgcgg ccagatgcca ctacgaagga ggtgaaggac tccctgggga agcagtggtc	840
tcagctctcg gacaaaaaga ggctgaaatg gattcataag gccctggagc agcggaaagga	900
gtacgaggag atcatgagag actatatcca gaagcaccca gagctgaaca tcagtgaagga	960
gggtatcacc aagtccaccc tcaccaaggc cgaacgccag ctcaaggaca agtttgacgg	1020

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gcgacccacc aagccaccte cgaacagcta ctgctgttac tgcgcagagc tcatggccaa 1080
catgaaggac gtgcccagca cagagcgcac ggtgctgtgc agccagcagt ggaagctgct 1140
gtcccagaag gagaaggacg cctatcacia gaagtgtgat cagaaaaaga aagattacga 1200
ggtggagctg ctccgtttcc tcgagagcct gcctgaggag gagcagcagc gggctcttggg 1260
ggaagagaag atgctgaaca tcaacaagaa gcaggccacc agccccgcct ccaagaagcc 1320
agcccaggaa gggggcaagg gcggctccga gaagcccaag cggcccgtgt cggccatggt 1380
catcttctcg gaggagaaac ggcggcagct gcaggaggag cggcctgagc tctccgagag 1440
cgagctgacc cgcctgctgg cccgaatgtg gaacgacctg tctgagaaga agaaggccaa 1500
gtacaaggcc cgagaggcgg cgctcaaggc tcagtcggag aggaagcccc gcggggagcg 1560
cgaggaacgg ggcaagctgc ccgagtcccc caaaagagct gaggagatct ggcaacagag 1620
cgttatcggc gactacctgg cccgcttcaa gaatgaccgg gtgaaggcct tgaaagccat 1680
ggaaatgacc tggaataaca tggaaaagaa ggagaaactg atgtggatta agaaggcagc 1740
cgaagaccaa aagcgatatg agagagagct gagtgagatg cgggcacctc cagctgctac 1800
aaattcttcc aagaagatga aattccaggg agaaccacaag aagcctccca tgaacggtta 1860
ccagaagtcc tcccaggagc tgctgtccaa tggggagctg aaccacctgc cgctgaagga 1920
gcgcatggtg gagatcggca gtgctggca gcgcatctcc cagagccaga aggagcacta 1980
caaaaagctg gccgaggagc agcaaaagca gtacaagggtg cacctggacc tctgggttaa 2040
gagcctgtct ccccaggacc gtgcagcata taaagagtac atctccaata aacgtaagag 2100
catgaccaag ctgcgaggcc caaaccacca atccagccgg actactctgc agtccaagtc 2160
ggagtccgag gaggatgatg aagaggatga ggatgacgag gacgaggatg aagaagagga 2220
agatgatgag aatggggact cctctgaaga tggcggcgac tcctctgagt ccagcagcga 2280
ggacgagagc gaggatgggg atgagaatga agaggatgac gaggacgaag acgacgacga 2340
ggatgacgat gaggatgaag ataatgagtc cgagggcagc agctccagct cctcctcctt 2400
aggggactcc tcagactttg actccaactg aggcttagcc ccaccccagg ggagccaggg 2460
agagcccagg agctcccctc cccaactgac cacctttgtt tcttccccat gttctgtccc 2520
ttgccccctt ggctcccccc actttctttc tttcttttaa aaaaaaaaaa aaaaactcga 2580
g

```

&lt;210&gt; 67

&lt;211&gt; 764

&lt;212&gt; PRT

&lt;213&gt; Homo sapien

&lt;400&gt; 67

```

Met Asn Gly Glu Ala Asp Cys Pro Thr Asp Leu Glu Met Ala Ala Pro
1          5          10          15
Lys Gly Gln Asp Arg Trp Ser Gln Glu Asp Met Leu Thr Leu Leu Glu
20          25          30
Cys Met Lys Asn Asn Leu Pro Ser Asn Asp Ser Ser Lys Phe Lys Thr
35          40          45
Thr Glu Ser His Met Asp Trp Glu Lys Val Ala Phe Lys Asp Phe Ser
50          55          60
Gly Asp Met Cys Lys Leu Lys Trp Val Glu Ile Ser Asn Glu Val Arg
65          70          75          80
Lys Phe Arg Thr Leu Thr Glu Leu Ile Leu Asp Ala Gln Glu His Val
85          90          95
Lys Asn Pro Tyr Lys Gly Lys Lys Leu Lys Lys His Pro Asp Phe Pro
100          105          110
Lys Lys Pro Leu Thr Pro Tyr Phe Arg Phe Phe Met Glu Lys Arg Ala
115          120          125
Lys Tyr Ala Lys Leu His Pro Glu Met Ser Asn Leu Asp Leu Thr Lys
130          135          140
Ile Leu Ser Lys Lys Tyr Lys Glu Leu Pro Glu Lys Lys Lys Met Lys
145          150          155          160
Tyr Ile Gln Asp Phe Gln Arg Glu Lys Gln Glu Phe Glu Arg Asn Leu

```

				165					170				175			
Ala	Arg	Phe	Arg	Glu	Asp	His	Pro	Asp	Leu	Ile	Gln	Asn	Ala	Lys	Lys	
			180					185					190			
Ser	Asp	Ile	Pro	Glu	Lys	Pro	Lys	Thr	Pro	Gln	Gln	Leu	Trp	Tyr	Thr	
		195					200					205				
His	Glu	Lys	Lys	Val	Tyr	Leu	Lys	Val	Arg	Pro	Asp	Ala	Thr	Thr	Lys	
	210					215					220					
Glu	Val	Lys	Asp	Ser	Leu	Gly	Lys	Gln	Trp	Ser	Gln	Leu	Ser	Asp	Lys	
225					230				235						240	
Lys	Arg	Leu	Lys	Trp	Ile	His	Lys	Ala	Leu	Glu	Gln	Arg	Lys	Glu	Tyr	
			245					250					255			
Glu	Glu	Ile	Met	Arg	Asp	Tyr	Ile	Gln	Lys	His	Pro	Glu	Leu	Asn	Ile	
			260					265					270			
Ser	Glu	Glu	Gly	Ile	Thr	Lys	Ser	Thr	Leu	Thr	Lys	Ala	Glu	Arg	Gln	
	275					280						285				
Leu	Lys	Asp	Lys	Phe	Asp	Gly	Arg	Pro	Thr	Lys	Pro	Pro	Pro	Asn	Ser	
	290					295					300					
Tyr	Ser	Leu	Tyr	Cys	Ala	Glu	Leu	Met	Ala	Asn	Met	Lys	Asp	Val	Pro	
305					310					315					320	
Ser	Thr	Glu	Arg	Met	Val	Leu	Cys	Ser	Gln	Gln	Trp	Lys	Leu	Leu	Ser	
			325						330					335		
Gln	Lys	Glu	Lys	Asp	Ala	Tyr	His	Lys	Lys	Cys	Asp	Gln	Lys	Lys	Lys	
			340					345					350			
Asp	Tyr	Glu	Val	Glu	Leu	Leu	Arg	Phe	Leu	Glu	Ser	Leu	Pro	Glu	Glu	
	355					360						365				
Glu	Gln	Gln	Arg	Val	Leu	Gly	Glu	Glu	Lys	Met	Leu	Asn	Ile	Asn	Lys	
	370					375					380					
Lys	Gln	Ala	Thr	Ser	Pro	Ala	Ser	Lys	Lys	Pro	Ala	Gln	Glu	Gly	Gly	
385					390					395					400	
Lys	Gly	Gly	Ser	Glu	Lys	Pro	Lys	Arg	Pro	Val	Ser	Ala	Met	Phe	Ile	
			405					410					415			
Phe	Ser	Glu	Glu	Lys	Arg	Arg	Gln	Leu	Gln	Glu	Glu	Arg	Pro	Glu	Leu	
			420					425				430				
Ser	Glu	Ser	Glu	Leu	Thr	Arg	Leu	Leu	Ala	Arg	Met	Trp	Asn	Asp	Leu	
	435					440						445				
Ser	Glu	Lys	Lys	Lys	Ala	Lys	Tyr	Lys	Ala	Arg	Glu	Ala	Ala	Leu	Lys	
	450					455					460					
Ala	Gln	Ser	Glu	Arg	Lys	Pro	Gly	Gly	Glu	Arg	Glu	Glu	Arg	Gly	Lys	
465					470					475					480	
Leu	Pro	Glu	Ser	Pro	Lys	Arg	Ala	Glu	Glu	Ile	Trp	Gln	Gln	Ser	Val	
			485					490						495		
Ile	Gly	Asp	Tyr	Leu	Ala	Arg	Phe	Lys	Asn	Asp	Arg	Val	Lys	Ala	Leu	
			500					505					510			
Lys	Ala	Met	Glu	Met	Thr	Trp	Asn	Asn	Met	Glu	Lys	Lys	Glu	Lys	Leu	
	515						520					525				
Met	Trp	Ile	Lys	Lys	Ala	Ala	Glu	Asp	Gln	Lys	Arg	Tyr	Glu	Arg	Glu	
	530					535					540					
Leu	Ser	Glu	Met	Arg	Ala	Pro	Pro	Ala	Ala	Thr	Asn	Ser	Ser	Lys	Lys	
545					550					555					560	
Met	Lys	Phe	Gln	Gly	Glu	Pro	Lys	Lys	Pro	Pro	Met	Asn	Gly	Tyr	Gln	
			565					570					575			
Lys	Phe	Ser	Gln	Glu	Leu	Leu	Ser	Asn	Gly	Glu	Leu	Asn	His	Leu	Pro	
			580					585					590			
Leu	Lys	Glu	Arg	Met	Val	Glu	Ile	Gly	Ser	Arg	Trp	Gln	Arg	Ile	Ser	
	595					600						605				



Gln	Ser	Gln	Lys	Glu	His	Tyr	Lys	Lys	Leu	Ala	Glu	Glu	Gln	Gln	Lys
610						615					620				
Gln	Tyr	Lys	Val	His	Leu	Asp	Leu	Trp	Val	Lys	Ser	Leu	Ser	Pro	Gln
625					630					635					640
Asp	Arg	Ala	Ala	Tyr	Lys	Glu	Tyr	Ile	Ser	Asn	Lys	Arg	Lys	Ser	Met
				645					650					655	
Thr	Lys	Leu	Arg	Gly	Pro	Asn	Pro	Lys	Ser	Ser	Arg	Thr	Thr	Leu	Gln
			660					665					670		
Ser	Lys	Ser	Glu	Ser	Glu	Glu	Asp	Asp	Glu	Glu	Asp	Glu	Asp	Asp	Glu
		675					680				685				
Asp	Glu	Asp	Glu	Glu	Glu	Glu	Asp	Asp	Glu	Asn	Gly	Asp	Ser	Ser	Glu
	690					695				700					
Asp	Gly	Gly	Asp	Ser	Ser	Glu	Ser	Ser	Ser	Glu	Asp	Glu	Ser	Glu	Asp
705					710					715					720
Gly	Asp	Glu	Asn	Glu	Glu	Asp	Asp	Glu	Asp	Glu	Asp	Asp	Asp	Glu	Asp
			725					730						735	
Asp	Asp	Glu	Asp	Glu	Asp	Asn	Glu	Ser	Glu	Gly	Ser	Ser	Ser	Ser	Ser
		740					745						750		
Ser	Ser	Leu	Gly	Asp	Ser	Ser	Asp	Phe	Asp	Ser	Asn				
	755						760								

&lt;210&gt; 68

&lt;211&gt; 434

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 68

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ccaatcgcat	ctgcaaagtg	ttggcgggtca	atcaagagaa	cgagcagctt	atggaagact	180
atgagaagct	ggccagtgat	ctgttggagt	ggatccgccc	caccatccca	tggttgagga	240
atcgggtgcc	tgagaacacc	atgcatgcca	tgcagcagaa	gctggaggac	ttccgagact	300
atagacgcct	gcacaagccg	cccaaggtgc	aggagaagtg	ccagctggag	atcaacttta	360
acacgctgca	gaccaaactg	cggctcagca	accggcctgc	cttcatgccc	tccgagggca	420
ggatggtctc	ggat					434

&lt;210&gt; 69

&lt;211&gt; 244

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 69

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ttatgtgctg	accttcctc	cactattgtc	ctgtgacctt	gccaaatccc	cctttgtgag	180
aaacacccaa	gaatgatcaa	taaaaataa	attaatttag	gaaaaaaaaa	aaaaaaaaact	240
cgag						244

&lt;210&gt; 70

&lt;211&gt; 437

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 70

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35

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cttggtccct ggatccagcg tcggccagcc cagagcccgt gccgcacatc cttgcgtcct 120
ccaggcagtg ggaccccgcg agctgcacgt ccctggggcac ggacaagtgt gaggcactgt 180
tggggctgtg ccagggtgcg ggtgggctgc cccctttctc agaaccttcc agcctggtgc 240
cgtggccccc aggccggagt cttcctaagg ctgtgaggcc acccctgtcc tggcctccgt 300
tctcgcagca gcagacctg cccgtgatga gcggggaggc ccttggttgg ctgggcccagg 360
ctgggtccct ggccatgggg gctgcacctc tgggggagcc agccaaggag gaccccatgc 420
tggcgcagga agccggg 437

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<210> 71  
 <211> 271  
 <212> DNA  
 <213> Homo sapien

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<400> 71
gcgcagagtt ctgtcgtcca ccatcgagtg aggaagagag cattgggttcc cctgagatag 60
aagagatggc tctcttcagt gccagttctc catacattaa cccgatcatc ccctttactg 120
gaccaatcca aggagggctg caggagggac ttcagggtgac cctccagggg actaccgaga 180
gttttgcaca aaagtttgtg gtgaactttt cagaacagct tcaatggaga tgacttggcc 240
ttccacttca accccggtta tgaggaagga g 271

```

<210> 72  
 <211> 290  
 <212> DNA  
 <213> Homo sapien

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<400> 72
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ctgggtgccct ctcttgctgc gaggactcgg cccaggggctc gggcccgcgc aaggccccta 120
cgggtggccga ggggtcccagc tcctgccttc ggcggaacgt gatcagcgag agggagcgca 180
ggaagcggat gtcggtgagc tgtgagcgtc tgcggggcct gctgccccag ttcgatggcc 240
ggcgggagga catggcctcg gtcttgagga tgtctgttgc aattcctgcg 290

```

<210> 73  
 <211> 144  
 <212> PRT  
 <213> Homo sapien

```

<400> 73
Lys Met Leu Asp Ala Glu Asp Ile Val Gly Thr Ala Arg Pro Asp Glu
 1           5           10          15
Lys Ala Ile Met Thr Tyr Val Ser Ser Phe Tyr His Ala Phe Ser Gly
          20          25          30
Ala Gln Lys Ala Glu Thr Ala Ala Asn Arg Ile Cys Lys Val Leu Ala
          35          40          45
Val Asn Gln Glu Asn Glu Gln Leu Met Glu Asp Tyr Glu Lys Leu Ala
          50          55          60
Ser Asp Leu Leu Glu Trp Ile Arg Arg Thr Ile Pro Trp Leu Glu Asn
65          70          75          80
Arg Val Pro Glu Asn Thr Met His Ala Met Gln Gln Lys Leu Glu Asp
          85          90          95
Phe Arg Asp Tyr Arg Arg Leu His Lys Pro Pro Lys Val Gln Glu Lys
          100         105         110
Cys Gln Leu Glu Ile Asn Phe Asn Thr Leu Gln Thr Lys Leu Arg Leu
          115         120         125
Ser Asn Arg Pro Ala Phe Met Pro Ser Glu Gly Arg Met Val Ser Asp

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130 135 140

<210> 74  
 <211> 64  
 <212> PRT  
 <213> Homo sapien

<400> 74  
 Gly Ser Met Leu Val Glu Ser His His His Ser Leu Ile Ser Ser Thr  
 1 5 10 15  
 Gln Gly His Lys His Cys Gly Arg Pro Gln Gly Pro Leu Pro Arg Lys  
 20 25 30  
 Thr Arg Asp Leu Cys Ser Leu Val Tyr Val Leu Thr Phe Pro Pro Leu  
 35 40 45  
 Leu Ser Cys Asp Pro Ala Lys Ser Pro Phe Val Arg Asn Thr Gln Glu  
 50 55 60

<210> 75  
 <211> 145  
 <212> PRT  
 <213> Homo sapien

<400> 75  
 Gly Thr Gly Ala Ser Ser Gly Thr Arg Thr Pro Asp Val Lys Ala Phe  
 1 5 10 15  
 Leu Glu Ser Pro Trp Ser Leu Asp Pro Ala Ser Ala Ser Pro Glu Pro  
 20 25 30  
 Val Pro His Ile Leu Ala Ser Ser Arg Gln Trp Asp Pro Ala Ser Cys  
 35 40 45  
 Thr Ser Leu Gly Thr Asp Lys Cys Glu Ala Leu Leu Gly Leu Cys Gln  
 50 55 60  
 Val Arg Gly Gly Leu Pro Pro Phe Ser Glu Pro Ser Ser Leu Val Pro  
 65 70 75 80  
 Trp Pro Pro Gly Arg Ser Leu Pro Lys Ala Val Arg Pro Pro Leu Ser  
 85 90 95  
 Trp Pro Pro Phe Ser Gln Gln Gln Thr Leu Pro Val Met Ser Gly Glu  
 100 105 110  
 Ala Leu Gly Trp Leu Gly Gln Ala Gly Ser Leu Ala Met Gly Ala Ala  
 115 120 125  
 Pro Leu Gly Glu Pro Ala Lys Glu Asp Pro Met Leu Ala Gln Glu Ala  
 130 135 140  
 Gly  
 145

<210> 76  
 <211> 69  
 <212> PRT  
 <213> Homo sapien

<400> 76  
 Ala Glu Phe Cys Arg Pro Pro Ser Ser Glu Glu Glu Ser Ile Gly Ser  
 1 5 10 15  
 Pro Glu Ile Glu Glu Met Ala Leu Phe Ser Ala Gln Ser Pro Tyr Ile  
 20 25 30  
 Asn Pro Ile Ile Pro Phe Thr Gly Pro Ile Gln Gly Gly Leu Gln Glu

37

35 40 45  
 Gly Leu Gln Val Thr Leu Gln Gly Thr Thr Glu Ser Phe Ala Gln Lys  
 50 55 60  
 Phe Val Val Asn Phe  
 65

<210> 77  
 <211> 96  
 <212> PRT  
 <213> Homo sapien

<400> 77  
 Glu Pro Tyr Pro Glu Val Ser Arg Ile Pro Thr Val Arg Gly Cys Asn  
 1 5 10 15  
 Gly Ser Leu Ser Gly Ala Leu Ser Cys Cys Glu Asp Ser Ala Gln Gly  
 20 25 30  
 Ser Gly Pro Pro Lys Ala Pro Thr Val Ala Glu Gly Pro Ser Ser Cys  
 35 40 45  
 Leu Arg Arg Asn Val Ile Ser Glu Arg Glu Arg Arg Lys Arg Met Ser  
 50 55 60  
 Leu Ser Cys Glu Arg Leu Arg Ala Leu Leu Pro Gln Phe Asp Gly Arg  
 65 70 75 80  
 Arg Glu Asp Met Ala Ser Val Leu Glu Met Ser Val Ala Ile Pro Ala  
 85 90 95

<210> 78  
 <211> 2076  
 <212> DNA  
 <213> Homo sapien

<400> 78  
 agaaaaagtc tatgttttgca gaaatacaga tccaagacaa agacaggatg ggcactgctg 60  
 gaaaagttat taaatgcaaa gcagctgtgc tttgggagca gaagcaaccc ttctccattg 120  
 aggaaataga agttgcccc ccaaagacta aagaagttcg cattaagatt ttggccacag 180  
 gaatctgtcg cacagatgac catgtgataa aaggaacaat ggtgtccaag tttccagtga 240  
 ttgtgggaca tgaggcaact gggattgtag agagcattgg agaaggagt actacagtga 300  
 aaccaggtga caaagtcac cctctctttc tgccacaatg tagagaatgc aatgcttgct 360  
 gcaacccaga tggcaacctt tgcattagga gcatattac tggtcgtgga gtactggctg 420  
 atggcaccac cagatttaca tgcaagggca aaccagtcca ccacttcacg aacaccagta 480  
 catttaccga gtacacagtg gtggatgaat cttctgttgc taagattgat gatgcagctc 540  
 ctcttgagaa agtctgttta attggctgtg ggttttccac tggatatggc gctgctgtta 600  
 aaactggcaa ggtcaaacct ggttccactt gcgtcgtctt tggcctgaga ggagttggcc 660  
 tgtcagtcac catgggctgt aagtcagctg gtgcatctag gatcattggg attgacctca 720  
 acaaagacaa atttgagaag gccatggctg taggtgccac tgagtgtatc agtcccaagg 780  
 actctaccaa acccatcagt gaggtgctgt cagaaatgac aggcaacaac gtgggataca 840  
 cttttgaagt tattgggcat cttgaaacca tgattgatgc cctggcatcc tgccacatga 900  
 actatgggac cagcgtgggt gtaggagttc ctccatcagc caagatgctc acctatgacc 960  
 cgatgttgct cttcactgga cgcacatgga agggatgtgt ctttggaggt ttgaaaagca 1020  
 gagatgatgt cccaaaacta gtgactgagt tcctggcaaa gaaatttgac ctggaccagt 1080  
 tgataactca tgtcttacca tttaaaaaaa tcagtgaagg atttgagctg ctcaattcag 1140  
 gacaaagcat tcgaacggtc ctgacgtttt gagatccaaa gtggcaggag gtctgtgttg 1200  
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 cacaataca agcataagta gaagatttgt tgaagacata gaacccttat aaagaattat 1320  
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 aatatttttg atttacattt tgtaaggcta taattgtatc ttttaagaaa acatacactt 1440

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taacacattg	aaactattat	tttttagatt	tgaatataaa	tgtatttttt	aaacacttgt	1620
tatgagttaa	cttggattac	attttgaaat	cagttcattc	catgatgcat	attactggat	1680
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tcattacata	acttgggtgaa	actgaaaaag	tatatcatat	gggtacacaa	ggctatttgc	1800
cagcatatat	taatatttta	gaaaatattc	cttttgtaat	actgaatata	aacatagagc	1860
tagaatcata	ttatcatact	tatcataatg	ttcaatttga	tacagtagaa	ttgcaagtcc	1920
ttaagtcctt	attcactgtg	cttagtagtg	actccattta	ataaaaagtg	tttttagttt	1980
ttaacaacta	cactgatgta	tttatatata	tttataacat	gttaaaaatt	tttaaggaaa	2040
ttaaaaatta	tataaaaaaa	aaaaaaaaaa	ctcgag			2076

&lt;210&gt; 79

&lt;211&gt; 2790

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 79

aagcagttga	gtaggcagaa	aaaagaacct	cttcattaag	gattaaaatg	tataggccag	60
cacgtgtaac	ttcgacttca	agattttctga	atccatatgt	agtatgtttc	attgtcgtcg	120
caggggtagt	gatcctggca	gtcaccatag	ctctacttgt	ttacttttta	gcttttgatc	180
aaaaatctta	cttttatagg	agcagttttc	aactcctaaa	tgttgaatat	aatagtcagt	240
taaattcacc	agctacacag	gaatacagga	ctttgagtgg	aagaattgaa	tctctgatta	300
ctaaaacatt	caaagaatca	aatttaagaa	atcagttcat	cagagctcat	gttgccaaac	360
tgaggcaaga	tggtagtggt	gtgagagcgg	atgttgtcat	gaaatttcaa	ttcactagaa	420
ataacaatgg	agcatcaatg	aaaagcagaa	ttgagtctgt	tttacgacaa	atgctgaata	480
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agagaatcct	tggaggcact	gaggctgagg	agggaagctg	gccgtggcaa	gtcagtcctg	660
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gagccatctt	gtctggaatg	ctgtgtgctg	gagtacctca	aggtggagtg	gacgcatgtc	1140
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ggatagtaag	ctggggagat	cagtgtggcc	tgccggataa	gccaggagtg	tatactcgag	1260
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acatagtact	ttttaacaac	aaaataataa	ttttaagaat	gaaaaattta	atcatcggga	2160
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aatgaaaaaa	aaaaaaaaaa	aaaactcgag				2790

&lt;210&gt; 80

&lt;211&gt; 1460

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 80

ctcaaagcag	ttgagtaggc	agaaaaaaga	acctcttcat	taaggattaa	aatgtatagg	60
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aaactgaggc	aagatggtag	tgggtgtgaga	gcggatgttg	tcatgaaatt	tcaattcact	420
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atccctgttg	caaagtctgt	atgcagggtg	gcctgtctta	aattccaaag	ctttacattt	1380
caactgaaaa	agaaactaga	aatgtcctaa	tttaacatct	tgttacataa	atatgggtta	1440
acaaaaaaaa	aaaaaaaaaa					1460

&lt;210&gt; 81

&lt;211&gt; 386

&lt;212&gt; PRT

&lt;213&gt; Homo sapien

&lt;400&gt; 81

Met	Phe	Ala	Glu	Ile	Gln	Ile	Gln	Asp	Lys	Asp	Arg	Met	Gly	Thr	Ala
1				5				10					15		
Gly	Lys	Val	Ile	Lys	Cys	Lys	Ala	Ala	Val	Leu	Trp	Glu	Gln	Lys	Gln
			20				25						30		
Pro	Phe	Ser	Ile	Glu	Glu	Ile	Glu	Val	Ala	Pro	Pro	Lys	Thr	Lys	Glu
			35				40						45		



40

Val	Arg	Ile	Lys	Ile	Leu	Ala	Thr	Gly	Ile	Cys	Arg	Thr	Asp	Asp	His
50						55				60					
Val	Ile	Lys	Gly	Thr	Met	Val	Ser	Lys	Phe	Pro	Val	Ile	Val	Gly	His
65					70				75					80	
Glu	Ala	Thr	Gly	Ile	Val	Glu	Ser	Ile	Gly	Glu	Gly	Val	Thr	Thr	Val
			85						90					95	
Lys	Pro	Gly	Asp	Lys	Val	Ile	Pro	Leu	Phe	Leu	Pro	Gln	Cys	Arg	Glu
			100					105					110		
Cys	Asn	Ala	Cys	Arg	Asn	Pro	Asp	Gly	Asn	Leu	Cys	Ile	Arg	Ser	Asp
		115					120					125			
Ile	Thr	Gly	Arg	Gly	Val	Leu	Ala	Asp	Gly	Thr	Thr	Arg	Phe	Thr	Cys
	130					135					140				
Lys	Gly	Lys	Pro	Val	His	His	Phe	Met	Asn	Thr	Ser	Thr	Phe	Thr	Glu
145					150					155					160
Tyr	Thr	Val	Val	Asp	Glu	Ser	Ser	Val	Ala	Lys	Ile	Asp	Asp	Ala	Ala
				165					170					175	
Pro	Pro	Glu	Lys	Val	Cys	Leu	Ile	Gly	Cys	Gly	Phe	Ser	Thr	Gly	Tyr
			180					185					190		
Gly	Ala	Ala	Val	Lys	Thr	Gly	Lys	Val	Lys	Pro	Gly	Ser	Thr	Cys	Val
		195					200				205				
Val	Phe	Gly	Leu	Arg	Gly	Val	Gly	Leu	Ser	Val	Ile	Met	Gly	Cys	Lys
	210					215					220				
Ser	Ala	Gly	Ala	Ser	Arg	Ile	Ile	Gly	Ile	Asp	Leu	Asn	Lys	Asp	Lys
225					230					235				240	
Phe	Glu	Lys	Ala	Met	Ala	Val	Gly	Ala	Thr	Glu	Cys	Ile	Ser	Pro	Lys
				245					250					255	
Asp	Ser	Thr	Lys	Pro	Ile	Ser	Glu	Val	Leu	Ser	Glu	Met	Thr	Gly	Asn
			260				265						270		
Asn	Val	Gly	Tyr	Thr	Phe	Glu	Val	Ile	Gly	His	Leu	Glu	Thr	Met	Ile
		275					280					285			
Asp	Ala	Leu	Ala	Ser	Cys	His	Met	Asn	Tyr	Gly	Thr	Ser	Val	Val	Val
	290					295					300				
Gly	Val	Pro	Pro	Ser	Ala	Lys	Met	Leu	Thr	Tyr	Asp	Pro	Met	Leu	Leu
305					310					315				320	
Phe	Thr	Gly	Arg	Thr	Trp	Lys	Gly	Cys	Val	Phe	Gly	Gly	Leu	Lys	Ser
				325					330					335	
Arg	Asp	Asp	Val	Pro	Lys	Leu	Val	Thr	Glu	Phe	Leu	Ala	Lys	Lys	Phe
			340					345					350		
Asp	Leu	Asp	Gln	Leu	Ile	Thr	His	Val	Leu	Pro	Phe	Lys	Lys	Ile	Ser
		355					360					365			
Glu	Gly	Phe	Glu	Leu	Leu	Asn	Ser	Gly	Gln	Ser	Ile	Arg	Thr	Val	Leu
	370					375					380				
Thr	Phe														
385															

&lt;210&gt; 82

&lt;211&gt; 418

&lt;212&gt; PRT

&lt;213&gt; Homo sapien

&lt;400&gt; 82

Met	Tyr	Arg	Pro	Ala	Arg	Val	Thr	Ser	Thr	Ser	Arg	Phe	Leu	Asn	Pro
1				5				10					15		
Tyr	Val	Val	Cys	Phe	Ile	Val	Val	Ala	Gly	Val	Val	Ile	Leu	Ala	Val
			20					25					30		

Thr Ile Ala Leu Leu Val Tyr Phe Leu Ala Phe Asp Gln Lys Ser Tyr  
 35 40 45  
 Phe Tyr Arg Ser Ser Phe Gln Leu Leu Asn Val Glu Tyr Asn Ser Gln  
 50 55 60  
 Leu Asn Ser Pro Ala Thr Gln Glu Tyr Arg Thr Leu Ser Gly Arg Ile  
 65 70 75 80  
 Glu Ser Leu Ile Thr Lys Thr Phe Lys Glu Ser Asn Leu Arg Asn Gln  
 85 90 95  
 Phe Ile Arg Ala His Val Ala Lys Leu Arg Gln Asp Gly Ser Gly Val  
 100 105 110  
 Arg Ala Asp Val Val Met Lys Phe Gln Phe Thr Arg Asn Asn Asn Gly  
 115 120 125  
 Ala Ser Met Lys Ser Arg Ile Glu Ser Val Leu Arg Gln Met Leu Asn  
 130 135 140  
 Asn Ser Gly Asn Leu Glu Ile Asn Pro Ser Thr Glu Ile Thr Ser Leu  
 145 150 155 160  
 Thr Asp Gln Ala Ala Ala Asn Trp Leu Ile Asn Glu Cys Gly Ala Gly  
 165 170 175  
 Pro Asp Leu Ile Thr Leu Ser Glu Gln Arg Ile Leu Gly Gly Thr Glu  
 180 185 190  
 Ala Glu Glu Gly Ser Trp Pro Trp Gln Val Ser Leu Arg Leu Asn Asn  
 195 200 205  
 Ala His His Cys Gly Gly Ser Leu Ile Asn Asn Met Trp Ile Leu Thr  
 210 215 220  
 Ala Ala His Cys Phe Arg Ser Asn Ser Asn Pro Arg Asp Trp Ile Ala  
 225 230 235 240  
 Thr Ser Gly Ile Ser Thr Thr Phe Pro Lys Leu Arg Met Arg Val Arg  
 245 250 255  
 Asn Ile Leu Ile His Asn Asn Tyr Lys Ser Ala Thr His Glu Asn Asp  
 260 265 270  
 Ile Ala Leu Val Arg Leu Glu Asn Ser Val Thr Phe Thr Lys Asp Ile  
 275 280 285  
 His Ser Val Cys Leu Pro Ala Ala Thr Gln Asn Ile Pro Pro Gly Ser  
 290 295 300  
 Thr Ala Tyr Val Thr Gly Trp Gly Ala Gln Glu Tyr Ala Gly His Thr  
 305 310 315 320  
 Val Pro Glu Leu Arg Gln Gly Gln Val Arg Ile Ile Ser Asn Asp Val  
 325 330 335  
 Cys Asn Ala Pro His Ser Tyr Asn Gly Ala Ile Leu Ser Gly Met Leu  
 340 345 350  
 Cys Ala Gly Val Pro Gln Gly Gly Val Asp Ala Cys Gln Gly Asp Ser  
 355 360 365  
 Gly Gly Pro Leu Val Gln Glu Asp Ser Arg Arg Leu Trp Phe Ile Val  
 370 375 380  
 Gly Ile Val Ser Trp Gly Asp Gln Cys Gly Leu Pro Asp Lys Pro Gly  
 385 390 395 400  
 Val Tyr Thr Arg Val Thr Ala Tyr Leu Asp Trp Ile Arg Gln Gln Thr  
 405 410 415  
 Gly Ile

&lt;210&gt; 83

&lt;211&gt; 418

&lt;212&gt; PRT

&lt;213&gt; Homo sapien

<400> 83

Met	Tyr	Arg	Pro	Ala	Arg	Val	Thr	Ser	Thr	Ser	Arg	Phe	Leu	Asn	Pro	1	5	10	15
Tyr	Val	Val	Cys	Phe	Ile	Val	Val	Ala	Gly	Val	Val	Ile	Leu	Ala	Val	20	25	30	
Thr	Ile	Ala	Leu	Leu	Val	Tyr	Phe	Leu	Ala	Phe	Asp	Gln	Lys	Ser	Tyr	35	40	45	
Phe	Tyr	Arg	Ser	Ser	Phe	Gln	Leu	Leu	Asn	Val	Glu	Tyr	Asn	Ser	Gln	50	55	60	
Leu	Asn	Ser	Pro	Ala	Thr	Gln	Glu	Tyr	Arg	Thr	Leu	Ser	Gly	Arg	Ile	65	70	75	80
Glu	Ser	Leu	Ile	Thr	Lys	Thr	Phe	Lys	Glu	Ser	Asn	Leu	Arg	Asn	Gln	85	90	95	
Phe	Ile	Arg	Ala	His	Val	Ala	Lys	Leu	Arg	Gln	Asp	Gly	Ser	Gly	Val	100	105	110	
Arg	Ala	Asp	Val	Val	Met	Lys	Phe	Gln	Phe	Thr	Arg	Asn	Asn	Asn	Gly	115	120	125	
Ala	Ser	Met	Lys	Ser	Arg	Ile	Glu	Ser	Val	Leu	Arg	Gln	Met	Leu	Asn	130	135	140	
Asn	Ser	Gly	Asn	Leu	Glu	Ile	Asn	Pro	Ser	Thr	Glu	Ile	Thr	Ser	Leu	145	150	155	160
Thr	Asp	Gln	Ala	Ala	Ala	Asn	Trp	Leu	Ile	Asn	Glu	Cys	Gly	Ala	Gly	165	170	175	
Pro	Asp	Leu	Ile	Thr	Leu	Ser	Glu	Gln	Arg	Ile	Leu	Gly	Gly	Thr	Glu	180	185	190	
Ala	Glu	Glu	Gly	Ser	Trp	Pro	Trp	Gln	Val	Ser	Leu	Arg	Leu	Asn	Asn	195	200	205	
Ala	His	His	Cys	Gly	Gly	Ser	Leu	Ile	Asn	Asn	Met	Trp	Ile	Leu	Thr	210	215	220	
Ala	Ala	His	Cys	Phe	Arg	Ser	Asn	Ser	Asn	Pro	Arg	Asp	Trp	Ile	Ala	225	230	235	240
Thr	Ser	Gly	Ile	Ser	Thr	Thr	Phe	Pro	Lys	Leu	Arg	Met	Arg	Val	Arg	245	250	255	
Asn	Ile	Leu	Ile	His	Asn	Asn	Tyr	Lys	Ser	Ala	Thr	His	Glu	Asn	Asp	260	265	270	
Ile	Ala	Leu	Val	Arg	Leu	Glu	Asn	Ser	Val	Thr	Phe	Thr	Lys	Asp	Ile	275	280	285	
His	Ser	Val	Cys	Leu	Pro	Ala	Ala	Thr	Gln	Asn	Ile	Pro	Pro	Gly	Ser	290	295	300	
Thr	Ala	Tyr	Val	Thr	Gly	Trp	Gly	Ala	Gln	Glu	Tyr	Ala	Gly	His	Thr	305	310	315	320
Val	Pro	Glu	Leu	Arg	Gln	Gly	Gln	Val	Arg	Ile	Ile	Ser	Asn	Asp	Val	325	330	335	
Cys	Asn	Ala	Pro	His	Ser	Tyr	Asn	Gly	Ala	Ile	Leu	Ser	Gly	Met	Leu	340	345	350	
Cys	Ala	Gly	Val	Pro	Gln	Gly	Gly	Val	Asp	Ala	Cys	Gln	Gly	Asp	Ser	355	360	365	
Gly	Gly	Pro	Leu	Val	Gln	Glu	Asp	Ser	Arg	Arg	Leu	Trp	Phe	Ile	Val	370	375	380	
Gly	Ile	Val	Ser	Trp	Gly	Asp	Gln	Cys	Gly	Leu	Pro	Asp	Lys	Pro	Gly	385	390	395	400
Val	Tyr	Thr	Arg	Val	Thr	Ala	Tyr	Leu	Asp	Trp	Ile	Arg	Gln	Gln	Thr	405	410	415	
Gly	Ile																		

<210> 84  
 <211> 489  
 <212> DNA  
 <213> Homo sapien

<400> 84  
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 atcagctgga tgccgtttct aagtaccagg aagtcacaaa taatttggag ttgcaaaaag 120  
 aattacagag gagtttcatg gcactaagtc aagatattca gaaaacaata aagaagacag 180  
 cacgtcggga gcagcttatg agagaagaag ctgaacagaa acgtttaaaa actgtacttg 240  
 agctacagta tgttttggac aaattgggag atgatgaagt gcggactgac ctgaaacaag 300  
 gtttgaatgg agtgccaata ttgtccgaag aggagttgtc attgttggaat gaattctata 360  
 agctagtaga ccctgaacgg gacatgagct tgaggttgaa tgaacagtat gaacatgcct 420  
 ccattcacct gtgggacctg ctggaaggga aggaaaaacc tgtatgtgga accacctata 480  
 aagttctaa 489

<210> 85  
 <211> 304  
 <212> DNA  
 <213> Homo sapien

<400> 85  
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 acgcggacag cgtggccgag ctcggggagc agatcgacaa cctgcagcgg gtgaagcaga 120  
 agctggagaa ggagaagagc gagatgaaga tggagatcga tgacctcgct tgtaacatgg 180  
 aggtcatctc caaatctaag ggaaaccttg agaagatgtg ccgcacactg gaggaccaag 240  
 tgagtgaact gaagaccacg gaggaggaac agcagcggct gatcaatgaa ctgactgcgc 300  
 agag 304

<210> 86  
 <211> 296  
 <212> DNA  
 <213> Homo sapien

<400> 86  
 gaaaatcctt cttttgaatg ggaatctcca agcagttgaa ttgggcgaaa aaagaacctc 60  
 ttccttaagg attaaaatgt ttagggaac acgtgttact tccacttcca gatttctgaa 120  
 tccatagtgt gtatgtttcc ttgtcctccc aggggttggt atcctggcag tccccatagc 180  
 tctacttggt tacttttttag cttttgatca aaaatcttac ttttattgga gcaattttcc 240  
 actcccaaat gttgaatata atagtcctgt taattccccc gcttcaccgg gaattc 296

<210> 87  
 <211> 904  
 <212> DNA  
 <213> Homo sapien

<400> 87  
 gtgtccagga aacgattcat gaacataaca agcttgetgc aaattcagat catctcatgc 60  
 agattcaaaa atgtgagttg gtcttgatcc acacctaccc agttggtgaa gacagccttg 120  
 tatctgatcg ttctaaaaaa gagttgtccc cggttttaac cagtgaagtt catagtgttc 180  
 gtgcaggacg gcatcttgct accaaattga atattttagt acagcaacat tttgacttgg 240  
 cttcaactac tattacaaat attccaatga aggaagaaca gcatgctaac acatctgcc 300  
 attatgatgt ggagctactt catcaciaag atgcacatgt agatttcctg aaaagtgggt 360

attcgcatct	aggtggcggc	agtcgagaag	gctcgtttaa	agaaacaata	acattaaagt	420
ggtgtacacc	aaggacaaat	aacattgaat	tacactattg	tactggagct	tatcggattt	480
cacctgtaga	tgtaaatagt	agaccttcct	cctgccttac	taattttctt	ctaaatggtc	540
gttctgtttt	attggaacaa	ccacgaaagt	caggttctaa	agtcattagt	catatgctta	600
gtagccatgg	aggagagatt	tttttgcacg	tccttagcag	ttctcgatcc	attctagaag	660
atccaccttc	aattagtga	ggatgtggag	gaagagttac	agactaccgg	attacagatt	720
ttggtgaatt	tatgagggga	aaacagatta	actccttttc	tacacccag	atataaaatc	780
gatggaagtc	ttgaggtccc	tttggaaccg	agccaaaaga	tcagttaaaa	aaacataccc	840
gttactggcc	tatgatttca	aaaaccacc	atttttaaca	tgcaagcggg	agttccgtta	900
acca						904

&lt;210&gt; 88

&lt;211&gt; 387

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 88

cgtctctccc	ccagttttgcc	gttcacccgg	agcgcctggg	acttgccgat	agtgggtgacg	60
gcggcaacat	gtctgtggct	ttcgcgggcc	cgaggcagcg	aggcaagggg	gagatcactc	120
ccgctgcgat	tcagaagatg	ttggatgaca	ataaccatct	tattcagtgt	ataatggact	180
ctcagaataa	aggaaagacc	tcagagtgtt	ctcagtatca	gcagatgttg	cacacaaact	240
tggtatacct	tgctacaata	gcagattcta	atcaaaatat	gcagtctctt	ttaccagcac	300
caccacaca	gaatatgcct	atgggtcctg	gagggatgaa	tcagagcggg	cctccccac	360
ctccacgctc	tcacaacatg	ccttcaa				387

&lt;210&gt; 89

&lt;211&gt; 481

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 89

tgttcttggg	cctgcggtgc	tatagagcag	gctcttctag	gttggcagtt	gccatggaat	60
ctggacccaa	aatgtttggc	cccgtttgcc	tggtggaaaa	taacaatgag	cagctattgg	120
tgaaccagca	agctatacag	attcttgaaa	agattttctca	gccagtgggtg	gtggtggcca	180
ttgtaggact	gtaccgtaca	gggaaatcct	acttgatgaa	ccatctggca	ggacagaatc	240
atggcttccc	tctgggctcc	acgggtgcagt	ctgaaaccaa	gggcatctgg	atgtgggtgcg	300
tgccccaccc	atccaagcca	aaccacaccc	tggtccttct	ggacaccgaa	ggtctgggcg	360
atgtggaaaa	gggtgaccct	agaatgact	cctggatctt	tgccctgggt	gtgctcctgt	420
gcagcacctt	tgtctacaac	agcatgagca	ccatcaacca	ccaggccctg	gagcagctgc	480
a						481

&lt;210&gt; 90

&lt;211&gt; 491

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 90

tgaaaactgt	tcttggacct	gcggtgctat	agagcaggtt	ggcagttgcc	atggaatctg	60
gacccaaaat	gttggccccc	gtttgcctgg	tggaaaataa	caatgagcag	ctattgggtga	120
accagcaagc	tatacagatt	cttgaaaaga	tttctcagcc	agtgggtgggtg	gtggccattg	180
taggactgta	ccgtacaggg	aaatcctact	tgatgaacca	tctggcagga	cagaatcatg	240
gcttccctct	gggtccacg	gtgcagtctg	aaaccaaggg	catctggatg	tggtgcgtgc	300
cccacccatc	caagccaaac	cacaccctgg	tccttctgga	caccgaaggt	ctgggcgatg	360
tggaaaaggg	tgaccctaag	aatgactcct	ggatctttgc	cctggctgtg	ctcctgtgca	420
gcacctttgt	ctacaacagc	atgagcacca	tcaaccacca	agccctggag	cagctgcatt	480

atgtgacgga c

491

<210> 91  
 <211> 488  
 <212> DNA  
 <213> Homo sapien

&lt;400&gt; 91

ttcgacagtc agccgcatct tcttttgcgt cgccagccga gccacatcgc tcagacacca	60
tggggaaggt gaaggtcgga gtcaacggat ttggtcgtat tgggcgcctg gtcaccaggg	120
ctgcttttaa ctctggtaaa gtggatattg ttgccatcaa tgaccccttc attgacctca	180
actacatggt ttacatgttc caatatgatt ccacccatgg caaattccat ggcaccgtcg	240
aggctgagaa cgggaagctt gtcatcaatg gaaatcccat caccatcttc caggagcgag	300
atccctccaa aatcaagtgg ggcgatgctg gcgctgagta cgtcgtggag tccactggcg	360
tcttcaccac catggagaag gctggggctc atttgcaggg gggagccaaa agggatcatca	420
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acagcctc	488

<210> 92  
 <211> 384  
 <212> DNA  
 <213> Homo sapien

&lt;400&gt; 92

gacagtcagc cgcattcttct tttgcgtcgc cagccgagcc acatcgctca gacaccatgg	60
ggaaggtgaa ggtcggagtc aacggatttg gtcgtatttg gcgcctggtc accagggctg	120
cttttaactc tggtaaagtg gatattgttg ccatcaatga ccccttcatt gacctcaact	180
acatggttta catgttccaa tatgattcca cccatggcaa attccatggc accgtcgagg	240
ctgagaacgg gaagcttgtc atcaatggaa atcccatcac catcttccag gagcgagatc	300
cctccaaaat caagtggggc gatactggcg ctgagtagct cgtggagtcc actggcgtct	360
tcaccacccat ggagaaggct gggg	384

<210> 93  
 <211> 162  
 <212> PRT  
 <213> Homo sapien

&lt;400&gt; 93

Lys Gly Lys Leu Asp Asp Tyr Gln Glu Arg Met Asn Lys Gly Glu Arg	
1 5 10 15	
Leu Asn Gln Asp Gln Leu Asp Ala Val Ser Lys Tyr Gln Glu Val Thr	
20 25 30	
Asn Asn Leu Glu Phe Ala Lys Glu Leu Gln Arg Ser Phe Met Ala Leu	
35 40 45	
Ser Gln Asp Ile Gln Lys Thr Ile Lys Lys Thr Ala Arg Arg Glu Gln	
50 55 60	
Leu Met Arg Glu Glu Ala Glu Gln Lys Arg Leu Lys Thr Val Leu Glu	
65 70 75 80	
Leu Gln Tyr Val Leu Asp Lys Leu Gly Asp Asp Glu Val Arg Thr Asp	
85 90 95	
Leu Lys Gln Gly Leu Asn Gly Val Pro Ile Leu Ser Glu Glu Glu Leu	
100 105 110	Ser Leu Leu Asp Glu
Phe Tyr Lys Leu Val Asp Pro Glu Arg Asp Met	
115 120 125	
Ser Leu Arg Leu Asn Glu Gln Tyr Glu His Ala Ser Ile His Leu Trp	



46

130		135		140											
Asp	Leu	Leu	Glu	Gly	Lys	Glu	Lys	Pro	Val	Cys	Gly	Thr	Thr	Tyr	Lys
145					150					155					160
Val	Leu														

<210> 94  
 <211> 100  
 <212> PRT  
 <213> Homo sapien

<400> 94

Asp	Leu	Glu	Glu	Ala	Thr	Leu	Gln	His	Glu	Ala	Thr	Ala	Ala	Thr	Leu
1				5					10					15	
Arg	Lys	Lys	His	Ala	Asp	Ser	Val	Ala	Glu	Leu	Gly	Glu	Gln	Ile	Asp
			20					25					30		
Asn	Leu	Gln	Arg	Val	Lys	Gln	Lys	Leu	Glu	Lys	Glu	Lys	Ser	Glu	Met
		35					40					45			
Lys	Met	Glu	Ile	Asp	Asp	Leu	Ala	Cys	Asn	Met	Glu	Val	Ile	Ser	Lys
	50					55					60				
Ser	Lys	Gly	Asn	Leu	Glu	Lys	Met	Cys	Arg	Thr	Leu	Glu	Asp	Gln	Val
65					70				75					80	
Ser	Glu	Leu	Lys	Thr	Gln	Glu	Glu	Glu	Gln	Gln	Arg	Leu	Ile	Asn	Glu
				85					90					95	
Leu	Thr	Ala	Gln												
			100												

<210> 95  
 <211> 99  
 <212> PRT  
 <213> Homo sapien

<400> 95

Lys	Ile	Leu	Pro	Leu	Asn	Gly	Asn	Leu	Gln	Ala	Val	Glu	Leu	Gly	Glu
1				5					10					15	
Lys	Arg	Thr	Ser	Ser	Leu	Arg	Ile	Lys	Met	Phe	Arg	Ala	Thr	Arg	Val
			20					25					30		
Thr	Ser	Thr	Ser	Arg	Phe	Leu	Asn	Pro	Tyr	Val	Val	Cys	Phe	Leu	Val
		35					40					45			
Leu	Pro	Gly	Val	Val	Ile	Leu	Ala	Val	Pro	Ile	Ala	Leu	Leu	Val	Tyr
	50					55					60				
Phe	Leu	Ala	Phe	Asp	Gln	Lys	Ser	Tyr	Phe	Tyr	Trp	Ser	Asn	Phe	Pro
65					70				75					80	
Leu	Pro	Asn	Val	Glu	Tyr	Asn	Ser	Pro	Phe	Asn	Ser	Pro	Ala	Ser	Pro
				85					90					95	
Gly	Ile	Pro													

<210> 96  
 <211> 257  
 <212> PRT  
 <213> Homo sapien

<400> 96

Val	Gln	Glu	Thr	Ile	His	Glu	His	Asn	Lys	Leu	Ala	Ala	Asn	Ser	Asp
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Ile

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<210> 97
<211> 128
<212> PRT
<213> Homo sapien
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<400> 97															
Ser	Leu	Pro	Gln	Phe	Ala	Val	His	Pro	Glu	Arg	Ser	Gly	Leu	Ala	Asp
1				5					10					15	
Ser	Gly	Asp	Gly	Gly	Asn	Met	Ser	Val	Ala	Phe	Ala	Ala	Pro	Arg	Gln
			20					25					30		
Arg	Gly	Lys	Gly	Glu	Ile	Thr	Pro	Ala	Ala	Ile	Gln	Lys	Met	Leu	Asp
		35					40					45			
Asp	Asn	Asn	His	Leu	Ile	Gln	Cys	Ile	Met	Asp	Ser	Gln	Asn	Lys	Gly
	50					55					60				
Lys	Thr	Ser	Glu	Cys	Ser	Gln	Tyr	Gln	Gln	Met	Leu	His	Thr	Asn	Leu
65					70					75					80
Val	Tyr	Leu	Ala	Thr	Ile	Ala	Asp	Ser	Asn	Gln	Asn	Met	Gln	Ser	Leu
				85					90					95	
Leu	Pro	Ala	Pro	Pro	Thr	Gln	Asn	Met	Pro	Met	Gly	Pro	Gly	Gly	Met
			100					105					110		
Asn	Gln	Ser	Gly	Pro	Pro	Pro	Pro	Pro	Arg	Ser	His	Asn	Met	Pro	Ser

125

<400> 98

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<210> 99
<211> 147
<212> PRT
<213> Homo sapien
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<400>. 99

[illegible]

49

<210> 100  
 <211> 124  
 <212> PRT  
 <213> Homo sapien

<400> 100  
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 20 25 30  
 Ile Asn Asp Pro Phe Ile Asp Leu Asn Tyr Met Val Tyr Met Phe Gln  
 35 40 45  
 Tyr Asp Ser Thr His Gly Lys Phe His Gly Thr Val Glu Ala Glu Asn  
 50 55 60  
 Gly Lys Leu Val Ile Asn Gly Asn Pro Ile Thr Ile Phe Gln Glu Arg  
 65 70 75 80  
 Asp Pro Ser Lys Ile Lys Trp Gly Asp Ala Gly Ala Glu Tyr Val Val  
 85 90 95  
 Glu Ser Thr Gly Val Phe Thr Thr Met Glu Lys Ala Gly Ala His Leu  
 100 105 110  
 Gln Gly Gly Ala Lys Arg Val Ile Ile Ser Ala Pro  
 115 120

<210> 101  
 <211> 127  
 <212> PRT  
 <213> Homo sapien

<400> 101  
 Gln Ser Ala Ala Ser Ser Phe Ala Ser Pro Ala Glu Pro His Arg Ser  
 1 5 10 15  
 Asp Thr Met Gly Lys Val Lys Val Gly Val Asn Gly Phe Gly Arg Ile  
 20 25 30  
 Gly Arg Leu Val Thr Arg Ala Ala Phe Asn Ser Gly Lys Val Asp Ile  
 35 40 45  
 Val Ala Ile Asn Asp Pro Phe Ile Asp Leu Asn Tyr Met Val Tyr Met  
 50 55 60  
 Phe Gln Tyr Asp Ser Thr His Gly Lys Phe His Gly Thr Val Glu Ala  
 65 70 75 80  
 Glu Asn Gly Lys Leu Val Ile Asn Gly Asn Pro Ile Thr Ile Phe Gln  
 85 90 95  
 Glu Arg Asp Pro Ser Lys Ile Lys Trp Gly Asp Thr Gly Ala Glu Tyr  
 100 105 110  
 Val Val Glu Ser Thr Gly Val Phe Thr Thr Met Glu Lys Ala Gly  
 115 120 125

<210> 102  
 <211> 1225  
 <212> DNA  
 <213> Homo sapien

<400> 102  
 atggcggcgc ggtcgtcgtc ggggggtggcg gcggcagagg gggcggcggc cctggcggca 60  
 gcggagacgg cagccgtgac ggtggcagcg gcggcgcggg acctgggcct gggggaatga 120

ggcgggccgcg	gcggggccagc	ggcgggagccg	tgtagcggag	aagctcccc	tccctgcttc	180
ccttgggccga	gccggggggcg	cgcgcgcacg	cggccgtcca	gagcgggctc	cccacccctc	240
gactcctgcg	acccgcaccg	cacccccacc	cgggcccggg	ggatgatgaa	gctcaagtcg	300
aaccagaccc	gcacctacga	cggcgacggc	tacaagaagc	gggcccgcag	cctgtgtttc	360
cgcagcgaga	gcgaggagga	gggtgtactc	gtgagcagta	gtcgccatcc	agacagatgg	420
attgtccctg	gaggaggcat	ggagcccag	gaggagccaa	gtgtggcagc	agttcgtgaa	480
gtctgtgagg	aggctggagt	aaaagggaca	ttgggaagat	tagttggaat	ttttgagaac	540
caggagagga	agcacaggac	gtatgtctat	gtgtctcattg	tcactgaagt	gctggaagac	600
tgggaagatt	cagttaacat	tggaaggag	agggaatggt	ttaaaataga	agacgccata	660
aaagtgtctg	agtatcacia	acccgtgcag	gcatcatatt	ttgaaacatt	gaggcaaggc	720
tactcagcca	acaatggcac	cccagtcgtg	gccaccacat	actcggtttc	tgctcagagc	780
tcgatgtcag	gcatcagatg	actgaagact	tcctgtgaaga	gaaatggaaa	ttggaaacta	840
gactgaagtg	caaattcttc	ctctcacctc	ggctcttttc	acttctcaca	ggcctcctct	900
ttcaaataag	gcatgggtggg	cagcaaagaa	agggtgtatt	gataatgttg	ctgtttgggtg	960
ttaagtgatg	gggctttttc	ttctgttttt	attgaggggtg	gggggtgggtg	gtgtaatttg	1020
taagtacttt	tgtgcatgat	ctgtccctcc	ctcttcccac	ccctgcagtc	ctctgaagag	1080
aggccaacag	ccttccctctg	ccttggattc	tgaagtgttc	ctgtttgtct	tatcctggcc	1140
ctggccagac	gttttctttg	atttttaatt	tttttttttt	attaaaagat	accagtatga	1200
gaaaaaaaaa	aaaaaaaaaac	tcgag				1225

&lt;210&gt; 103

&lt;211&gt; 741

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 103

agaaacctca	atcggtattca	gcaaagggaat	gggtgttatta	tcactacata	ccaaatgtta	60
atcaataact	ggcagcaact	ttcaagcttt	agggggccaag	agtttgtgtg	ggactatgtc	120
atcctcgatg	aagcacataa	aataaaaacc	tcattctacta	agtcagcaat	atgtgctcgt	180
gctattcctg	caagtaatcg	cctcctcctc	acaggaaccc	caatccagaa	taattttacaa	240
gaactatggg	ccctatttga	ttttgcttgt	caagggtccc	tgctgggaac	attaaaaact	300
tttaagatgg	agtatgaaaa	tcctattact	agagcaagag	agaaggatgc	taccccagga	360
gaaaaagcct	tgggatttta	aatatctgaa	aacttaatgg	caatcataaa	accctatttt	420
ctcaggagga	ctaaagaaga	cgtacagaag	aaaaagtcaa	gcaacccaga	ggccagactt	480
aatgaaaaga	atccagatgt	tgatgccatt	tgtgaaatgc	cttccctttc	caggagaaat	540
gatttaatta	tttgatacag	acttgtgcct	ttacaagaag	aaatatacag	gaaatttgtg	600
tcttttagatc	atatcaagga	gttgctaattg	gagacgcgct	cacctttggc	tgagctaggt	660
gtcttaaaga	agctgtgtga	tcattcctagg	ctgctgtctg	cacgggcttg	ttgtttgcta	720
aattcttggga	cattctctgc	t				741

&lt;210&gt; 104

&lt;211&gt; 321

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 104

ttgtcttgcg	tcattcaaaga	caccaaactg	ctgtgctata	aaagttecaa	ggaccagcag	60
cctcagatgg	aactgccact	ccaaggctgt	aacattacgt	acatcccga	agacagcaaa	120
aagaagaagc	acgagctgaa	gattactcag	cagggcacgg	acccgcttgt	tctcgccgtc	180
cagagcaagg	aacaggccga	gcagtggctg	aaggatgatca	aagaagccta	cagtgggtgt	240
agtggccccg	tggattcaga	gtgtcctcct	ccaccaagct	ccccggtgca	caaggcagaa	300
ctggagaaga	aactgtcttc	a				321

&lt;210&gt; 105

&lt;211&gt; 389

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 105

cagcactggc	cacactataa	aattcaggtt	cagaaaaaca	gggtaagtca	cagacagcaa	60
cgcttccagc	at ttat tttc	tttgcaccca	tgggcaattt	gagaaaattt	accttttagaa	120
cgaactctgt	t aaaggtaca	gacagtacaa	tactttttat	tcagaaggtt	tctgcataaa	180
ggtgatagtc	ttttgactta	atatattatt	gtctcctgcc	ttgtgtttct	ggaatgaatg	240
aaggtcatta	tttagaagat	aatctggggt	gtattttgtg	cgtcagattg	aattttcatt	300
gcacatgcta	cttaatgtct	ttaccaaata	ataacaaagg	gaaagaaaac	caaatataga	360
tgtataataa	ggaaaagctg	gcctataga				389

&lt;210&gt; 106

&lt;211&gt; 446

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 106

gccacatttg	ccctgggtcat	agtttaaaca	ccaggtcctg	tgtcacatct	ttttgggtgcc	60
acaagtatca	ctccattggt	cagagagtaa	tgtattagtt	ctgcccatt	cattcttcac	120
ttttatttct	tccatttcat	tagcatttat	atcagctcaa	gaagttaagg	ttagaaaatt	180
ttccacttca	aatttttcagt	acagaaatgt	gctgtgatgt	ttgacaagac	tatttcatag	240
taagtgaagt	aatgtttatt	ggcctctgct	ctcctctgtg	tcagacctag	gaagcctgag	300
gattacttag	ttgttctgtc	tctgggtcca	caggcagaat	ttggcccatc	caaagactgg	360
ccaagtgcc	aaaaaaggcc	tgattaggcc	ctgaaattca	gtgaaattct	gcctgaagaa	420
acctcttatt	gaatttgaaa	accata				446

&lt;210&gt; 107

&lt;211&gt; 467

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 107

ccgccgctgc	cgctgccttc	ctgggattgg	agtctcgagc	tttcttcgtt	cgttcgccgg	60
cggttctgcg	cccttctcgc	gcctcggggc	tgcgaggctg	gggaaggggt	tggagggggc	120
tggtgatcgc	cgcgtttaag	ttgcgctcgg	ggcgcccatg	tcggccggcg	aggctgagcg	180
cctagtgtcg	gagctgagcg	gcgggaccgg	aggggatgag	gaggaagagt	ggctctatgg	240
cgatgaagat	gaagttgaaa	ggccagaaga	agaaaatgcc	agtgtctaac	ctccatctgg	300
aattgaagat	gaaactgctg	aaaatgggtg	accaaaaccg	aaagtgactg	agaccgaaga	360
tgatagtgat	agtgacagcg	atgatgatga	agatgatgtg	catgtcacta	taggagacat	420
taaaacggga	gcaccacagt	atgggagtta	tggtacagca	cctgtaa		467

&lt;210&gt; 108

&lt;211&gt; 491

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 108

gaaagataca	acttccccaa	cccaaaccgg	tttgtggagg	acgacatgga	taagaatgaa	60
atcgctctcg	ttgcgtaccg	ttaccgcagg	tggaagcttg	gagatgatat	tgaccttatt	120
gtccgttgtg	agcacgatgg	cgatcatgact	ggagccaacg	gggaagtgtc	cttcatcaac	180
atcaagacac	tcaatgagtg	ggattccagg	cactgtaatg	gcgttgactg	gcgtcagaag	240
ctggactctc	agcgaggggc	tgtcattgcc	acggagctga	agaacaacag	ctacaagtgt	300
gcccgggtgga	cctgctgtgc	tttgctggct	ggatctgagt	acctcaagct	tggttatgtg	360
tctcggtacc	acgtgaaaga	ctcctcacgc	cacgtcatcc	taggcacca	gcagttcaag	420



cctaattgagt ttgccagcca gatcaacctg agcgtggaga atgcctgagg catttttacgc 480  
 tgcgtcattg a 491

<210> 109  
 <211> 489  
 <212> DNA  
 <213> Homo sapien

<400> 109  
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 actaagtgac taagggggcag gtagtataca gtgtggataa gcaggacaaa ggggtgattc 120  
 acatcccagg caggacagag caggagatca tgagatttca tcactcagga tggcttgtga 180  
 tttatttttat tttattcttt tttttttttg agatggagtc tcactcttgc ccaggctgga 240  
 gtgcagtggg gcgatcttgg ctactgcaa cctctgcctc ctgggttcaa gcagttctcc 300  
 tgcctcagcc tcccaagtag ctgggattac aggcgtccgc caccatgccc agccaatttt 360  
 tgtactttta gtagagatgg ggtttcacca tgttggccag gctgggtctcg aactcctgac 420  
 ctcaggtgat ccactcgct cggcctccca aagtgctggg attataggca tgcgccacca 480  
 tgcccgggc 489

<210> 110  
 <211> 391  
 <212> DNA  
 <213> Homo sapien

<400> 110  
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 gtctgagtac ctccggccgc gcgcacgctg catcgccggag ccaggctgcc gctgtcccag 120  
 tggagttcca ggagcaccac ctgagtgagg tgcagaatat ggcatctgag gagaagctgg 180  
 agcaggtgct gagttccatg aaggagaaca aagtggccat cattggaaag attcataccc 240  
 cgatggagta taaggggggag ctagcctcct atgatatgcg gctgaggcgt aagttggact 300  
 tatttgccaa cgtaatccat gtgaagtcac ttcctgggta tatgactcgg cacaacaatc 360  
 tagacctggg gatcattcga gagcagacag a 391

<210> 111  
 <211> 172  
 <212> PRT  
 <213> Homo sapien

<400> 111  
 Met Met Lys Leu Lys Ser Asn Gln Thr Arg Thr Tyr Asp Gly Asp Gly  
 1 5 10 15  
 Tyr Lys Lys Arg Ala Ala Cys Leu Cys Phe Arg Ser Glu Ser Glu Glu  
 20 25 30  
 Glu Val Leu Leu Val Ser Ser Ser Arg His Pro Asp Arg Trp Ile Val  
 35 40 45  
 Pro Gly Gly Gly Met Glu Pro Glu Glu Glu Pro Ser Val Ala Ala Val  
 50 55 60  
 Arg Glu Val Cys Glu Glu Ala Gly Val Lys Gly Thr Leu Gly Arg Leu  
 65 70 75 80  
 Val Gly Ile Phe Glu Asn Gln Glu Arg Lys His Arg Thr Tyr Val Tyr  
 85 90 95  
 Val Leu Ile Val Thr Glu Val Leu Glu Asp Trp Glu Asp Ser Val Asn  
 100 105 110  
 Ile Gly Arg Lys Arg Glu Trp Phe Lys Ile Glu Asp Ala Ile Lys Val  
 115 120 125

53

Leu	Gln	Tyr	His	Lys	Pro	Val	Gln	Ala	Ser	Tyr	Phe	Glu	Thr	Leu	Arg
130						135					140				
Gln	Gly	Tyr	Ser	Ala	Asn	Asn	Gly	Thr	Pro	Val	Val	Ala	Thr	Thr	Tyr
145					150					155					160
Ser	Val	Ser	Ala	Gln	Ser	Ser	Met	Ser	Gly	Ile	Arg				
				165					170						

&lt;210&gt; 112

&lt;211&gt; 247

&lt;212&gt; PRT

&lt;213&gt; Homo sapien

&lt;400&gt; 112

Arg	Asn	Leu	Asn	Arg	Ile	Gln	Gln	Arg	Asn	Gly	Val	Ile	Ile	Thr	Thr
1			5						10					15	
Tyr	Gln	Met	Leu	Ile	Asn	Asn	Trp	Gln	Gln	Leu	Ser	Ser	Phe	Arg	Gly
			20					25					30		
Gln	Glu	Phe	Val	Trp	Asp	Tyr	Val	Ile	Leu	Asp	Glu	Ala	His	Lys	Ile
		35					40					45			
Lys	Thr	Ser	Ser	Thr	Lys	Ser	Ala	Ile	Cys	Ala	Arg	Ala	Ile	Pro	Ala
	50					55					60				
Ser	Asn	Arg	Leu	Leu	Leu	Thr	Gly	Thr	Pro	Ile	Gln	Asn	Asn	Leu	Gln
65					70					75					80
Glu	Leu	Trp	Ser	Leu	Phe	Asp	Phe	Ala	Cys	Gln	Gly	Ser	Leu	Leu	Gly
				85					90					95	
Thr	Leu	Lys	Thr	Phe	Lys	Met	Glu	Tyr	Glu	Asn	Pro	Ile	Thr	Arg	Ala
			100					105					110		
Arg	Glu	Lys	Asp	Ala	Thr	Pro	Gly	Glu	Lys	Ala	Leu	Gly	Phe	Lys	Ile
		115					120					125			
Ser	Glu	Asn	Leu	Met	Ala	Ile	Ile	Lys	Pro	Tyr	Phe	Leu	Arg	Arg	Thr
	130					135					140				
Lys	Glu	Asp	Val	Gln	Lys	Lys	Lys	Ser	Ser	Asn	Pro	Glu	Ala	Arg	Leu
145					150					155					160
Asn	Glu	Lys	Asn	Pro	Asp	Val	Asp	Ala	Ile	Cys	Glu	Met	Pro	Ser	Leu
				165					170					175	
Ser	Arg	Arg	Asn	Asp	Leu	Ile	Ile	Trp	Ile	Arg	Leu	Val	Pro	Leu	Gln
			180					185					190		
Glu	Glu	Ile	Tyr	Arg	Lys	Phe	Val	Ser	Leu	Asp	His	Ile	Lys	Glu	Leu
		195					200					205			
Leu	Met	Glu	Thr	Arg	Ser	Pro	Leu	Ala	Glu	Leu	Gly	Val	Leu	Lys	Lys
	210					215					220				
Leu	Cys	Asp	His	Pro	Arg	Leu	Leu	Ser	Ala	Arg	Ala	Cys	Cys	Leu	Leu
225					230					235					240
Asn	Leu	Gly	Thr	Phe	Ser	Ala									
						245									

&lt;210&gt; 113

&lt;211&gt; 107

&lt;212&gt; PRT

&lt;213&gt; Homo sapien

&lt;400&gt; 113

Leu	Leu	Cys	Val	Ile	Lys	Asp	Thr	Lys	Leu	Leu	Cys	Tyr	Lys	Ser	Ser
1				5					10					15	
Lys	Asp	Gln	Gln	Pro	Gln	Met	Glu	Leu	Pro	Leu	Gln	Gly	Cys	Asn	Ile

54

			20					25					30				
Thr	Tyr	Ile	Pro	Lys	Asp	Ser	Lys	Lys	Lys	Lys	His	Glu	Leu	Lys	Ile		
		35					40					45					
Thr	Gln	Gln	Gly	Thr	Asp	Pro	Leu	Val	Leu	Ala	Val	Gln	Ser	Lys	Glu		
	50					55					60						
Gln	Ala	Glu	Gln	Trp	Leu	Lys	Val	Ile	Lys	Glu	Ala	Tyr	Ser	Gly	Cys		
65					70					75					80		
Ser	Gly	Pro	Val	Asp	Ser	Glu	Cys	Pro	Pro	Pro	Pro	Ser	Ser	Pro	Val		
				85					90					95			
His	Lys	Ala	Glu	Leu	Glu	Lys	Lys	Leu	Ser	Ser							
			100					105									

<210> 114  
 <211> 155  
 <212> PRT  
 <213> Homo sapien

			20					25					30				
Glu	Arg	Tyr	Asn	Phe	Pro	Asn	Pro	Asn	Pro	Phe	Val	Glu	Asp	Asp	Met		
1			5					10					15				
Asp	Lys	Asn	Glu	Ile	Ala	Ser	Val	Ala	Tyr	Arg	Tyr	Arg	Arg	Trp	Lys		
			20					25					30				
Leu	Gly	Asp	Asp	Ile	Asp	Leu	Ile	Val	Arg	Cys	Glu	His	Asp	Gly	Val		
	35					40					45						
Met	Thr	Gly	Ala	Asn	Gly	Glu	Val	Ser	Phe	Ile	Asn	Ile	Lys	Thr	Leu		
	50				55						60						
Asn	Glu	Trp	Asp	Ser	Arg	His	Cys	Asn	Gly	Val	Asp	Trp	Arg	Gln	Lys		
65					70				75						80		
Leu	Asp	Ser	Gln	Arg	Gly	Ala	Val	Ile	Ala	Thr	Glu	Leu	Lys	Asn	Asn		
				85					90					95			
Ser	Tyr	Lys	Leu	Ala	Arg	Trp	Thr	Cys	Cys	Ala	Leu	Leu	Ala	Gly	Ser		
			100					105						110			
Glu	Tyr	Leu	Lys	Leu	Gly	Tyr	Val	Ser	Arg	Tyr	His	Val	Lys	Asp	Ser		
	115					120						125					
Ser	Arg	His	Val	Ile	Leu	Gly	Thr	Gln	Gln	Phe	Lys	Pro	Asn	Glu	Phe		
	130					135					140						
Ala	Ser	Gln	Ile	Asn	Leu	Ser	Val	Glu	Asn	Ala							
145					150					155							

<210> 115  
 <211> 129  
 <212> PRT  
 <213> Homo sapien

			20					25					30				
Gly	Val	Arg	Trp	Leu	Thr	Arg	Ala	Leu	Val	Ser	Ala	Gly	Asn	Pro	Gly		
1			5					10					15				
Ala	Trp	Arg	Gly	Leu	Ser	Thr	Ser	Ala	Ala	Ala	His	Ala	Ala	Ser	Arg		
			20					25					30				
Ser	Gln	Ala	Ala	Val	Pro	Val	Glu	Phe	Gln	Glu	His	His	Leu	Ser			
	35					40					45						
Glu	Val	Gln	Asn	Met	Ala	Ser	Glu	Glu	Lys	Leu	Glu	Gln	Val	Leu	Ser		
	50					55					60						
Ser	Met	Lys	Glu	Asn	Lys	Val	Ala	Ile	Ile	Gly	Lys	Ile	His	Thr	Pro		
65					70					75					80		

55

Met Glu Tyr Lys Gly Glu Leu Ala Ser Tyr Asp Met Arg Leu Arg Arg  
                     85                    90                    95  
 Lys Leu Asp Leu Phe Ala Asn Val Ile His Val Lys Ser Leu Pro Gly  
                     100                    105                    110  
 Tyr Met Thr Arg His Asn Asn Leu Asp Leu Val Ile Ile Arg Glu Gln  
                     115                    120                    125  
 Thr

<210> 116  
 <211> 550  
 <212> DNA  
 <213> Homo sapien

<400> 116  
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 tggctcaccg ctgcctagag ccaaggagct catcctgaat gaccttcccg ccagcactcc 180  
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 gaggagcccc ctgactctgt ccagtcctct caccacgtcc ttcagcctgg gctcccacag 360  
 cactctcaac ggagacctct ccgtgcccag ctccctacgtc agcctccacc tgtcccccca 420  
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 ctccctccac 550

<210> 117  
 <211> 154  
 <212> DNA  
 <213> Homo sapien

<400> 117  
 ttctgagggg aagccgagtg gagtggggcga cccggcgggcg gtgacaatga gttttcttgg 60  
 aggcctttttt ggtcccatatt gtgagattga tgttgccctt aatgatgggg aaaccaggaa 120  
 aatggcagaa atgaaaactg aggatggcaa agta 154

<210> 118  
 <211> 449  
 <212> DNA  
 <213> Homo sapien

<400> 118  
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 cgcgcgctgg tgtcggcgca atgggtggcg gaggcgctgc gggccccgcg cgctgggcag 120  
 cctctgcagc tgetggacgc ctccctggtac ctgccgaagc tggggcgcgga cgcgcgacgc 180  
 gagttcgagg agcgcacat cccggggcgcc gctttcttcg acatcgacca gtgcagcgac 240  
 cgcacctcgc cctacgacca catgctgccc ggggcccagc atttcgcgga gtacgcaggc 300  
 cgcctggggcg tgggcgcggc caccacgtc gtgatctacg acgccagcga ccagggcctc 360  
 tactccgccc cgcgcgtctg gtggatgttc cgcgccttcg gccaccacgc cgtgtcactg 420  
 cttgatggcg gcctccgcca ctggctgcg 449

<210> 119  
 <211> 642  
 <212> DNA  
 <213> Homo sapien

&lt;400&gt; 119

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ctgtccaaac	cttcttctct	cctgtcaaca	gtggccagcc	ccccaactat	gagatgctca	120
aggaggagca	cgaggtggct	gtgctggggg	cgccccacaa	ccctgctccc	ccgacgtcca	180
ccgtgatcca	catccgcagc	gagacctccg	tgccccacca	tgctgctctg	tccctgttca	240
acaccctctt	catgaacccc	tgetgcctgg	gcttcatagc	atcgccctac	tccgtgaagt	300
ctagggacag	gaagatgggt	ggcgacgtga	ccggggccca	ggcctatgcc	tccaccgccca	360
agtgcctgaa	catctggggc	ctgattctgg	gcattcctcat	gaccattctg	ctcatcgtca	420
tcccagtgt	gatcttccag	gcctatggat	agatcaggag	gcattcactga	ggccaggagc	480
tctgcccatt	acctgtatcc	cacgtactcc	aacttccatt	cctcgccctg	cccccgagc	540
cgagtcctgt	atcagccctt	tatcctcaca	cgcttttcta	caatggcatt	caataaagtg	600
cacgtgtttc	tggtgaaaaa	aaaaaaaaaa	aaaaaactcg	ag		642

&lt;210&gt; 120

&lt;211&gt; 603

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 120

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gtcctccacc	ccgggaacag	ctccccctcc	caaagtgtg	accagcccgg	ccaccacacc	120
catgtccacc	atgtccacaa	tccacacctc	ctctactcca	gagaccaccc	acacctccac	180
agtgtgtgacc	accacagcca	ccatgacaag	ggccaccaat	tccacggcca	cacctctctc	240
cactctgggg	acgacccgga	tcctcactga	gctgaccaca	acagccacta	caactgcagc	300
cactggatcc	acggccaccc	tgtcctccac	cccaggggacc	acctggatcc	tcacagagcc	360
gagcactata	gccaccgtga	tggtgcccac	cggttccacg	gccaccgcct	cctccactct	420
gggaacagct	cacaccccca	aagtgggtgac	caccatggcc	actatgccc	cagccactgc	480
ctccacgggt	cccagctcgt	ccaccgtggg	gaccacccgc	accctgtcag	tgctccccag	540
cagcctgcca	accttcagcg	tgtccactgt	gtcctcctca	gtcctcacca	ccctgagacc	600
cac						603

&lt;210&gt; 121

&lt;211&gt; 178

&lt;212&gt; PRT

&lt;213&gt; Homo sapien

&lt;400&gt; 121

Ser	Glu	Pro	Pro	Ser	Pro	Ala	Thr	Thr	Pro	Cys	Gly	Lys	Val	Pro	Ile
1				5					10					15	
Cys	Ile	Pro	Ala	Arg	Arg	Asp	Leu	Val	Asp	Ser	Pro	Ala	Ser	Leu	Ala
			20					25					30		
Ser	Ser	Leu	Gly	Ser	Pro	Leu	Pro	Arg	Ala	Lys	Glu	Leu	Ile	Leu	Asn
		35					40					45			
Asp	Leu	Pro	Ala	Ser	Thr	Pro	Ala	Ser	Lys	Ser	Cys	Asp	Ser	Ser	Pro
	50					55					60				
Pro	Gln	Asp	Ala	Ser	Thr	Pro	Arg	Pro	Ser	Ser	Ala	Ser	His	Leu	Cys
65					70				75					80	
Gln	Leu	Ala	Ala	Lys	Pro	Ala	Pro	Ser	Thr	Asp	Ser	Val	Ala	Leu	Arg
			85					90					95		
Ser	Pro	Leu	Thr	Leu	Ser	Ser	Pro	Phe	Thr	Thr	Ser	Phe	Ser	Leu	Gly
			100					105					110		
Ser	His	Ser	Thr	Leu	Asn	Gly	Asp	Leu	Ser	Val	Pro	Ser	Ser	Tyr	Val
		115				120						125			
Ser	Leu	His	Leu	Ser	Pro	Gln	Val	Ser	Ser	Ser	Val	Val	Tyr	Gly	Arg

57

130		135		140
Ser Pro Val Met Ala Phe Glu Ser His Pro His Leu Arg Gly Ser Ser				
145		150		155
Val Ser Ser Ser Leu Pro Ser Ile Pro Gly Gly Lys Pro Ala Tyr Ser				160
	165		170	175
Phe His				

<210> 122  
 <211> 36  
 <212> PRT  
 <213> Homo sapien

<400> 122
Met Ser Phe Leu Gly Gly Phe Phe Gly Pro Ile Cys Glu Ile Asp Val
1 5 10 15
Ala Leu Asn Asp Gly Glu Thr Arg Lys Met Ala Glu Met Lys Thr Glu
20 25 30
Asp Gly Lys Val
35

<210> 123  
 <211> 136  
 <212> PRT  
 <213> Homo sapien

<400> 123
Met Ala Ser Pro Gln Leu Cys Arg Ala Leu Val Ser Ala Gln Trp Val
1 5 10 15
Ala Glu Ala Leu Arg Ala Pro Arg Ala Gly Gln Pro Leu Gln Leu Leu
20 25 30
Asp Ala Ser Trp Tyr Leu Pro Lys Leu Gly Arg Asp Ala Arg Arg Glu
35 40 45
Phe Glu Glu Arg His Ile Pro Gly Ala Ala Phe Phe Asp Ile Asp Gln
50 55 60
Cys Ser Asp Arg Thr Ser Pro Tyr Asp His Met Leu Pro Gly Ala Glu
65 70 75 80
His Phe Ala Glu Tyr Ala Gly Arg Leu Gly Val Gly Ala Ala Thr His
85 90 95
Val Val Ile Tyr Asp Ala Ser Asp Gln Gly Leu Tyr Ser Ala Pro Arg
100 105 110
Val Trp Trp Met Phe Arg Ala Phe Gly His His Ala Val Ser Leu Leu
115 120 125
Asp Gly Gly Leu Arg His Trp Leu
130 135

<210> 124  
 <211> 133  
 <212> PRT  
 <213> Homo sapien

<400> 124
Met Asn His Thr Val Gln Thr Phe Phe Ser Pro Val Asn Ser Gly Gln
1 5 10 15
Pro Pro Asn Tyr Glu Met Leu Lys Glu Glu His Glu Val Ala Val Leu



58

			20					25					30				
Gly	Ala	Pro	His	Asn	Pro	Ala	Pro	Pro	Thr	Ser	Thr	Val	Ile	His	Ile		
		35					40					45					
Arg	Ser	Glu	Thr	Ser	Val	Pro	Asp	His	Val	Val	Trp	Ser	Leu	Phe	Asn		
	50					55					60						
Thr	Leu	Phe	Met	Asn	Pro	Cys	Cys	Leu	Gly	Phe	Ile	Ala	Phe	Ala	Tyr		
65					70					75					80		
Ser	Val	Lys	Ser	Arg	Asp	Arg	Lys	Met	Val	Gly	Asp	Val	Thr	Gly	Ala		
				85					90					95			
Gln	Ala	Tyr	Ala	Ser	Thr	Ala	Lys	Cys	Leu	Asn	Ile	Trp	Ala	Leu	Ile		
			100					105					110				
Leu	Gly	Ile	Leu	Met	Thr	Ile	Leu	Leu	Ile	Val	Ile	Pro	Val	Leu	Ile		
	115						120					125					
Phe	Gln	Ala	Tyr	Gly													
	130																

<210> 125  
 <211> 195  
 <212> PRT  
 <213> Homo sapien

Thr	Thr	Ala	Thr	Thr	Thr	Ala	Ser	Thr	Gly	Ser	Thr	Ala	Thr	Pro	Ser		
1				5					10					15			
Ser	Thr	Pro	Gly	Thr	Ala	Pro	Pro	Pro	Lys	Val	Leu	Thr	Ser	Pro	Ala		
			20					25					30				
Thr	Thr	Pro	Met	Ser	Thr	Met	Ser	Thr	Ile	His	Thr	Ser	Ser	Thr	Pro		
		35					40					45					
Glu	Thr	Thr	His	Thr	Ser	Thr	Val	Leu	Thr	Thr	Thr	Ala	Thr	Met	Thr		
	50					55					60						
Arg	Ala	Thr	Asn	Ser	Thr	Ala	Thr	Pro	Ser	Ser	Thr	Leu	Gly	Thr	Thr		
65					70					75					80		
Arg	Ile	Leu	Thr	Glu	Leu	Thr	Thr	Thr	Ala	Thr	Thr	Thr	Ala	Ala	Thr		
				85					90					95			
Gly	Ser	Thr	Ala	Thr	Leu	Ser	Ser	Thr	Pro	Gly	Thr	Thr	Trp	Ile	Leu		
			100					105					110				
Thr	Glu	Pro	Ser	Thr	Ile	Ala	Thr	Val	Met	Val	Pro	Thr	Gly	Ser	Thr		
	115						120					125					
Ala	Thr	Ala	Ser	Ser	Thr	Leu	Gly	Thr	Ala	His	Thr	Pro	Lys	Val	Val		
	130					135					140						
Thr	Thr	Met	Ala	Thr	Met	Pro	Thr	Ala	Thr	Ala	Ser	Thr	Val	Pro	Ser		
145					150					155					160		
Ser	Ser	Thr	Val	Gly	Thr	Thr	Arg	Thr	Pro	Ala	Val	Leu	Pro	Ser	Ser		
				165					170					175			
Leu	Pro	Thr	Phe	Ser	Val	Ser	Thr	Val	Ser	Ser	Ser	Val	Leu	Thr	Thr		
			180					185					190				
Leu	Arg	Pro															
	195																

<210> 126  
 <211> 509  
 <212> DNA  
 <213> Homo sapien

<400> 126

gaattcggca	cgagccaagt	accccctgag	gaatctgcag	cctgcatctg	agtacaccgt	60
atccctcgtg	gccataaagg	gcaaccaaga	gagccccc	gccactggag	tctttaccac	120
actgcagcct	gggagctcta	ttccacctta	caacaccgag	gtgactgaga	ccaccattgt	180
gatcacatgg	acgcctgctc	caagaattgg	ttttaagctg	ggtgtacgac	caagccaggg	240
aggagaggca	ccacgagaag	tgacttcaga	ctcaggaagc	atcgttgtgt	ccggcttgac	300
tccaggagta	gaatacgtct	acaccatcca	agtcctgaga	gatggacagg	aaagagatgc	360
gccaattgta	aacaaagtgg	tgacaccatt	gtctccacca	acaaacttgc	atctggaggc	420
aaaccctgac	actggagtgc	tcacagtctc	ctggagagga	gcaccacccc	agacattact	480
gggtatagaa	ttaccacaac	ccctacaaa				509

&lt;210&gt; 127

&lt;211&gt; 500

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 127

gaattcggca	cgagccactg	atgtccgggg	agtcagccag	gagcttgggg	aaggggaagcg	60
cgcccccg	gccgggtccc	gagggctcga	tccgcatcta	cagcatgagg	ttctgcccgt	120
ttgctgagag	gacgcgtcta	gtcctgaagg	ccaaggggaat	caggcatgaa	gtcatcaata	180
tcaacctgaa	aaataagcct	gagtggttct	ttaagaaaaa	tcccttttgt	ctggtgccag	240
ttctggaaaa	cagtcagggg	cagctgatct	acgagtctgc	catcacctgt	gagtacctgg	300
atgaagcata	cccaggggaag	aagctgttgc	cggatgaccc	ctatgagaaa	gcttgccaga	360
agatgatctt	agagttgttt	tctaagggtgc	catccttggt	aggaagcttt	attagaagcc	420
aaaataaaga	agactatgct	ggcctaaaag	aagaatttcg	taaagaattt	accaagctag	480
aggaggttct	gactaataag					500

&lt;210&gt; 128

&lt;211&gt; 500

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 128

agctttcttc	tgctgccgct	cggtcacgct	tgtgcccga	ggaggaaaca	gtgacagacc	60
tggagactgc	agttctctat	ccttcacaca	gctctttcac	catgcctgga	tcacttcctt	120
tgaatgcaga	agcttgctgg	ccaaaagatg	tgggaattgt	tgcccttgag	atctattttc	180
cttctcaata	tgttgatcaa	gcagagttgg	aaaaatatga	tgggtgtagat	gctggaaagt	240
ataccattgg	cttggggccag	gccaagatgg	gcttctgcac	agatagagaa	gatattaact	300
ctctttgcat	gactgtgggt	cagaatctta	tggagagaaa	taacctttcc	tatgattgca	360
ttggggcggt	ggaagttgga	acagagacaa	tcatcgacaa	atcaaagtct	gtgaagacta	420
atgtgatgca	gctgtttgaa	gagtctggga	atacagatat	agaaggaatc	gacacaacta	480
atgcatgcta	tggaggcaca					500

&lt;210&gt; 129

&lt;211&gt; 497

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 129

gaattcggca	cgagcagagg	tctccagagc	cttctctctc	ctgtgcaaaa	tggcaactct	60
taaggaaaaa	ctcattgcac	cagttgcgga	agaagaggca	acagttccaa	acaataagat	120
cactgtagtg	ggtgttgga	aagttggtat	ggcgtgtgct	atcagcattc	tgggaaagtc	180
tctggctgat	gaacttgctc	ttgtggatgt	tttgggaagat	aagcttaaag	gagaaatgat	240
ggatctgcag	catgggagct	tatttcttca	gacacctaaa	attgtggcag	ataaagatta	300
ttctgtgacc	gccaattcta	agattgtagt	ggtaactgca	ggagtcctgc	agcaagaagg	360
ggagagtcgg	ctcaatctgg	tgcagagaaa	tgtaaatgtc	ttcaaattca	ttattcctca	420

gatcgtcaag tacagtcctg attgcatcat aattgtggtt tccaacccag tggacattct 480  
tacgtatggt acctgga 497

<210> 130

<211> 383

<212> DNA

<213> Homo sapien

<400> 130

gaattcggca	cgagggccgc	ggctgccgac	tgggtccccct	gccgctgtcg	ccaccatggc	60
tccgcaccgc	cccgcgcccgc	cgctgctttg	cgcgctgtcc	ctggcgctgt	gcgcgctgtc	120
gctgcccgtc	cgcgcgccca	ctgcgtcgcg	gggggcgctcc	caggcggggg	cgccccaggg	180
gcgggtgccc	gagggcgcg	ccaacagcat	ggtggtggaa	caccccgagt	tcctcaaggc	240
aggggaaggag	cctggcctgc	agatctggcg	tgtggagaaa	gttcgatctg	gtggcccgtg	300
cccaccaacc	tttatggaga	cttcttcacg	ggcgacgcct	acgtcatcct	gaagacagtg	360
cagcttaaga	acggaaaatc	ttg				383

<210> 131

<211> 509

<212> DNA

<213> Homo sapien

<400> 131

gaattcggca	cgagagtcag	ccgcattctc	ttttgcgtcg	ccagccgagc	cacatcgctc	60
agacaccatg	gggaagggtga	aggtcggagt	caacggattt	ggtcgtattg	ggcgccctgg	120
caccaggggt	gcttttaact	ctggtaaagt	ggatattgtt	gccatcaatg	accccttcat	180
tgacctcaac	tacatgggtt	acatgttcca	atatgattcc	acccatggca	aattccatgg	240
caccgtcaag	gctgagaacg	ggaagcttgt	catcaatgga	aatcccatca	ccatcttcca	300
ggagcgagat	ccctccaaaa	tcaagtgggg	cgatgctggc	gctgagtacg	tcgtggagtc	360
cactggccgt	cttcaccacc	atggagaagg	ctgggggtca	tttgcagggg	ggagccaaaa	420
gggtcatcat	ctctgcccc	tctgctgacg	cccccatgtt	cgtcatgggt	gtgaaccatg	480
agaagtatga	caacagcctc	aagatcatc				509

<210> 132

<211> 357

<212> DNA

<213> Homo sapien

<400> 132

gaattcggca	cgagtaagaa	gaagccccta	gaccacagct	ccacaccatg	gactggacct	60
ggaggatcct	cttcttggtg	gcagcagcaa	caggtgccca	ctcccagggt	caactgggtg	120
aatctgggtc	tgagttgaag	aagcctgggg	cctcagtga	ggtttcctgc	aaggcttctg	180
gacacatctt	cagtatctat	ggtttgaatt	gggtgcgaca	ggcccctgg	caaggccttg	240
agtggatggg	atggatcaaa	gtcgacactg	cgaacccaac	gtatgccag	ggcttcacag	300
gacgatttgt	cttctccctg	gacacctctg	tcagcacggc	atatctgcag	atcagca	357

<210> 133

<211> 468

<212> DNA

<213> Homo sapien

<400> 133

gaattcggca	cgaggcgccc	cgaaccgtcc	tcctgctgct	ctcggcgggc	ctggccctga	60
ccgagacctg	ggccggctcc	cactccatga	ggtatttcga	caccgccatg	tcccggcccc	120
gccgcgggga	gccccgcttc	atctcagtgg	gctacgtgga	cgacacgcag	ttcgtgaggt	180

tcgacagcga	cgccgcgagt	ccgagagagg	agccgcgggc	gccgtggata	gagcaggagg	240
ggccggagta	ttgggaccgg	aacacacaga	tcttcaagac	caacacacag	actgaccgag	300
agagcctgcg	gaacctgcgc	ggctactaca	accagagcga	ggccgggtct	cacaccctcc	360
agagcatgta	cggctgcgac	gtggggccgg	acgggcgctt	cctccgcggg	cataaccagt	420
acgcctacga	cggcaaggat	tacatcgccc	tgaacgagga	cctgcgct		468

<210> 134  
 <211> 214  
 <212> DNA  
 <213> Homo sapien

<400> 134						
gaattcggca	cgagctgcgt	cctgctgagc	tctgttctct	ccagcacctc	ccaacccact	60
agtgcctggg	tctcttgctc	caccaggaac	aagccaccat	gtctcgccag	tcaagtgtgt	120
ccttcgggag	cgggggcagt	cgtagcttca	gcaccgcctc	tgccatcacc	ccgtctgtct	180
cccgcaccag	cttcacctcc	gtgtcccggg	ccgg			214

<210> 135  
 <211> 355  
 <212> DNA  
 <213> Homo sapien

<400> 135						
gaattcggca	cgaggtgaac	aggacccgtc	gccatggggc	gtgtgatccg	tggacagagg	60
aagggcgccg	ggtctgtgtt	ccgcgcgcac	gtgaagcacc	gtaaaggcgc	tgcgcgcccg	120
cgcgccgtgg	atttcgctga	gcggcacggc	tacatcaagg	gcacgtctca	ggacatcatc	180
cacgacccgg	gccgcggcgc	gcccctcgcc	aaggtgggtc	tccgggatcc	gtatcggttt	240
aagaagcgga	cggagctgtt	cattgccgcc	gagggcattc	acacggggcca	gtttgtgtat	300
tgcggaaga	aggcccagct	caacattggc	aatgtgctcc	ctgtggggcac	catgc	355

<210> 136  
 <211> 242  
 <212> DNA  
 <213> Homo sapien

<400> 136						
gaattcggca	cgagccagct	cctaaccgcg	agtgatccgc	cagcctccgc	ctcccagagg	60
gcccggattg	cagacggagt	ctccttcaact	cagtgtctca	tggtgccccag	gctggagtgc	120
agtgggtgtg	tctcggctcg	ctacaacatc	cacctcccag	cagcctgcct	tggcctccca	180
aagtgccgag	attgcagctc	tctgcccggc	cgccaccctt	gtctgggaag	tgaggatgct	240
gt						242

<210> 137  
 <211> 424  
 <212> DNA  
 <213> Homo sapien

<400> 137						
gaattcggca	cgagcccaga	tcccagaggc	cgacagcgcc	cggcccagat	ccccacgcct	60
gccaggagca	agccgagagc	cagccggccg	gcgcactccg	actccgagca	gtctctgtcc	120
ttcgacccga	gccccgcgcg	ctttccggga	cccctgcccc	gcgggcagcg	ctgccaaacct	180
gccggccatg	gagaccccgt	cccagcggcg	cgccaccgcg	agcggggcgc	aggccagctc	240
cactccgctg	tcgcccaccc	gcacaccccg	gctgcaggag	aaggaggacc	tgaggagagc	300
caatgatcgc	ttggcggtct	acatcgaccg	tgtgcgctcg	ctggaaacgg	agaacgcagg	360
gctgcgcctt	cgcacacccg	agtctgaaga	ggtggtcagc	cgcgagggtg	ccggcatcaa	420

ggcc

424

<210> 138  
 <211> 448  
 <212> DNA  
 <213> Homo sapien

&lt;400&gt; 138

gaattcggca	cgagcctgtg	ttccaggagc	cgaatcagaa	atgtcatcct	caggcacgcc	60
agacttacct	gtcctactca	ccgatttgaa	gattcaatat	actaagatct	tcataaacia	120
tgaatggcat	gattcagtga	gtggcaagaa	atttcctgtc	tttaatcctg	caactgagga	180
ggagctctgc	caggtagaag	aaggagataa	ggaggatgtt	gacaaggcag	tgaaggccgc	240
aagacaggct	tttcagattg	gatccccgtg	gcgtactatg	gatgcttccg	agagggggcg	300
actattatac	aagttggctg	attttaatcga	aagagatcgt	ctgctgctgg	ccgacaatgg	360
agtcaatgaa	tgggtgaaaa	ctctattcca	atgcatatct	gaatgattta	gcaggctgca	420
tcaaaacatt	gcgctactgt	gcagggtg				448

<210> 139  
 <211> 510  
 <212> DNA  
 <213> Homo sapien

&lt;400&gt; 139

gaattcggca	cgagggttccg	tgcagctcac	ggagaagcga	atggacaaag	tcggcaagta	60
cccccaaggag	ctgcgcaagt	gctgcgagga	cggcatgcgg	gagaacccca	tgagggttctc	120
gtgccagcgc	cggaccctgt	tcattctcct	ggcgaggcgt	gcaagaaggt	cttcctggac	180
tgttgcaact	acatcacaga	gctgcggcgg	cagcacgcgc	gggccagcca	cctggcctgc	240
caggagtaac	ctggatgagg	acatcattgc	agaagagaac	atcgtttccc	gaagtgagtt	300
cccagagagc	tggctgtgga	acgttgagga	cttgaaagag	ccaccgaaaa	atggaatctc	360
tacgaagctc	atgaatatat	ttttgaaaga	ctccatcacc	acgtgggaga	ttctggctgt	420
gagcatgtcg	gacaagaaag	ggatctgtgt	ggcagacccc	ttcgagggtca	cagtaatgca	480
ggacttcttc	atcgacctgc	ggctacccta				510

<210> 140  
 <211> 360  
 <212> DNA  
 <213> Homo sapien

&lt;400&gt; 140

gaattcggca	cgagcgggtaa	ctacccccggc	tgcgcacagc	tcggcgctcc	ttcccgtctc	60
ctcacacacc	ggcctcagcc	cgcaccggca	gtagaagatg	gtgaaagaaa	caacttacta	120
cgatgttttg	ggggtcaaac	ccaatgctac	tcaggaagaa	ttgaaaaagg	cttataggaa	180
actggctttg	aagtaccatc	ctgataagaa	cccaaataaa	ggagagaagt	ttaaacagat	240
ttctcaagct	tacgaagtgc	tctctgatgc	aaagaaaagg	gaattatatg	acaaaggagg	300
agaacaggca	attaaagagg	gtggagcagg	tggcggtttt	ggctccccca	tggacatctt	360

<210> 141  
 <211> 483  
 <212> DNA  
 <213> Homo sapien

&lt;400&gt; 141

gaattcggca	cgagagcaga	ggctgatctt	tgctggaaaa	cagctggaag	atgggctgca	60
ccctgtctga	ctacaacatc	cagaaagagt	ccaccctgca	cctgggtgctc	cgtctcagag	120
gtgggatgca	aatcttcgtg	aagacactca	ctggcaagac	catcaccctt	gagggtggagc	180

ccagtgcacac	catcgagaac	gtcaaagcaa	agatccagga	caaggaaggc	attcctcctg	240
accagcagag	gttgatcttt	gccggaaagc	agctggaaga	tgggcgcacc	ctgtctgact	300
acaacatcca	gaaagagtct	accctgcacc	tgggtgctccg	tctcagaggt	gggatgcaga	360
tcttcgtgaa	gaccctgact	ggtaagacca	tcaccctcga	ggtggagccc	agtgcacca	420
tcgagaatgt	caaggcaaag	atccaagata	aggaaggcat	tcctcctgat	cagcagaggt	480
tga						483

&lt;210&gt; 142

&lt;211&gt; 500

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 142

gaattcggca	cgaggcggcg	acgaccgccg	ggagcgtgtg	cagcggcggc	ggcgggaagtg	60
gccggcgagc	ccggtccccg	ccggcaccat	gcttcccttg	tcactgctga	agacgggtca	120
gaatcacccc	atggtggtgg	agctgaaaaa	tggggagacg	tacaatggac	acctggtgag	180
ctgcgacaac	tggatgaaca	ttaacctgcg	agaagtcatc	tgcacgtcca	gggacgggga	240
caagttctgg	cggatgcccg	agtgctacat	ccgcggcagc	accatcaagt	acctgcgcat	300
ccccgacgag	atcatcgaca	tgggtcaagga	ggaggtggtg	gccaagggcc	gcggccgcgg	360
aggcctgcag	cagcagaagc	agcagaaagg	ccgcggcatg	ggcggcgctg	gccgaggtgt	420
gtttggtggc	cggggccgag	gtgggatccc	gggcacaggc	agaagccagc	cagagaagaa	480
gcctggcaga	caggcgggca					500

&lt;210&gt; 143

&lt;211&gt; 400

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 143

gaattcggca	cgagctcgga	tgtcagcagg	cgtcccaacc	cagcaggaac	tggctcaatt	60
ctcagaagaa	agcgatcggc	cccagggcag	gaaggccggc	tccggtgcag	ggcgcgccgc	120
ctgcgggctg	cttcggggcca	gggtcgaccc	gagggccagc	gcaagcagcg	gcaacaggag	180
cgccaggagg	acatgaggct	ctgcctgcag	tcagcaactt	ggaatattca	gacttcagac	240
cagcatcaca	gattataacc	ctccgtaaat	catctgcac	ccagctccca	tcaaaagcca	300
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&lt;210&gt; 144

&lt;211&gt; 243

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 144

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&lt;210&gt; 145

&lt;211&gt; 450

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 145



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&lt;210&gt; 146

&lt;211&gt; 451

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 146

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&lt;210&gt; 147

&lt;211&gt; 400

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 147

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&lt;210&gt; 148

&lt;211&gt; 503

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 148

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&lt;210&gt; 149

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 <212> DNA  
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<400> 150

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 <212> DNA  
 <213> Homo sapien

<400> 151

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&lt;210&gt; 152

&lt;211&gt; 2179

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 152

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&lt;210&gt; 153

&lt;211&gt; 2109

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 153

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&lt;211&gt; 1411

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 154

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&lt;211&gt; 678

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 155

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&lt;211&gt; 2668

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 156

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&lt;211&gt; 2313

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 157

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&lt;211&gt; 2114

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 158

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 <213> Homo sapien

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&lt;210&gt; 163

&lt;211&gt; 432

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 163

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gctgcaacct	gaaggggacg	cagacagtgc	cggcggtctg	gccgtgccct	ctgagtgcct	180
ggacgccatg	gaggagcccg	accatggtgc	cctgctgctg	ctcccaggca	ggcctcaccc	240
ccatggccag	tctgtcatca	cggtgatcgg	gggcgaggag	cactttgagg	actacgggtga	300
aggcagtga	gcggagctgt	ccccagagac	cctatgcaac	gggcagctgg	gctgcagtga	360
ccccgctttc	ctcacgecca	gtccgacaaa	gcggctctcc	agcaagaagg	tggcaaggta	420
cctgcaccag	tc					432

&lt;210&gt; 164

&lt;211&gt; 395

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 164

gacacttgaa	tcattgggtga	cgttaaaaat	tttctgtatg	cctgggtgtgg	caaaaggaag	60
atgaccccat	cctatgaaat	tagagcagtg	gggaacaaaa	acaggcagaa	attcatgtgt	120
gaggttcagg	tggaagggtta	taattacact	ggcatgggaa	attccaccaa	taaaaaagat	180
gcacaaagca	atgctgccag	agactttgtt	aactatttgg	ttcgaataaa	tgaaataaag	240
agtgaagaag	ttccagcttt	tggggtagca	tctccgcccc	cacttactga	tactcctgac	300
actacagcaa	atgctgaagg	catcttggtg	acatcgaata	tgactttgat	aataaataacc	360
ggttcctgaa	aaaaaaaaaa	aaaaaaaaaac	tcgag			395

&lt;210&gt; 165

&lt;211&gt; 503

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 165

gaattcggca	ccaggaacgc	tcggtgagag	gcggaggagc	ggtaactacc	ccggttgccg	60
acagctcggc	gctccttccc	gctccctcac	acaccggcct	cagcccgcac	cggcagtga	120
agatggtgaa	agaaacaact	tactacgatg	ttttgggggt	caaaccctaat	gctactcagg	180
aagaattgaa	aaaggcttat	aggaaactgg	ccttgaagta	ccatcctgat	aagaaccctaa	240
atgaaggaga	gaagttttaa	cagatttctc	aagcttacga	agttctctct	gatgcaaaga	300
aaaggggaatt	atatgacaaa	ggaggagAAC	aggcaattaa	agaggggtgga	gcagggtggcg	360
gttttggtct	ccccatggac	atctttgata	tgtttttttg	aggaggagga	aggatgcaga	420
gagaaaggag	aggtaaaaat	gttgtagatc	agctctcagt	aaccctagaa	gacttatata	480
atggtgcaac	aagaaaactg	gct				503

&lt;210&gt; 166

<211> 893  
 <212> DNA  
 <213> Homo sapien

<400> 166

gaattcggca	cgagaggaac	ttctcttgac	gagaagagag	accaaggagg	ccaagcaggg	60
gctgggcccag	aggtgccaac	atgggggaaac	tgaggctcgg	ctcggaaggg	tgagagtgag	120
actacatctc	aaaaaaaaaa	aaaaaaaaaa	aaaagaaaga	aaagaaaaga	aaaaagaaag	180
aacggaagta	gttgtaggta	gtgggtatggt	ggtatgagtc	tgttttctgt	tacttataac	240
aacaacaaca	acaaaaaacg	ctgaaactgg	gtaatttata	aagaaaagga	aaaaaagcag	300
aaaaaaatca	ggaagaagag	aaaggaaaag	aagacaaata	aatgaaattt	atgtattaca	360
gttctgaagg	ctgagacatc	ccagggtcaag	ggtccacact	tggcgagggc	tttcttgctg	420
gtggagactc	tttgtggagt	cctgggacag	tgcagaagga	tcacgcctcc	ctaccgctcc	480
aagcccagcc	ctcagccatg	gcatgcccc	tggatcaggc	cattggcctc	ctcgtggcca	540
tcttccacaa	gtactccggc	agggagggtg	acaagcacac	cctgagcaag	aaggagctga	600
aggagctgat	ccagaaggag	ctcaccattg	gctcgaagct	gcaggatgct	gaaattgcaa	660
ggctgatgga	agacttggac	cggacaagag	accaggaggt	gaacttccag	gagtatgtca	720
ccttctctggg	ggccttggct	ttgatctaca	atgaagccct	caagggtctga	aaataaatag	780
ggaagatgga	gacaccctct	gggggtcctc	tctgagtcaa	atccagtggg	gggtaattgt	840
acaataaatt	tttttttggtc	aaatttataaa	aaaaaaaaaa	aaaaaaactc	gag	893

<210> 167  
 <211> 549  
 <212> DNA  
 <213> Homo sapien

<400> 167

gaattcggca	cgagcccaga	tcccagaggtc	cgacagcgcc	cggcccagat	ccccacgcct	60
gccaggagca	agccgagagc	cagccggccg	gcgcactccg	actccgagca	gtctctgtcc	120
ttcgacccga	gccccgcgcc	ctttccggga	cccctgcccc	gcggggcagcg	ctgccaacct	180
gccggccatg	gagaccccg	cccagcggcg	cgccaccgcg	agcggggcg	aggccagctc	240
cactccgctg	tcgcccaccc	gcatcacccg	gctgcaggag	aaggaggacc	tgaggagct	300
caatgatcgc	ttggcggtct	acatcgaccg	tgtgcgctcg	ctggaaacgg	agaacgcagg	360
gctgcgcctt	cgcacacccg	agtctgaaga	ggtgggtcagc	cgcgaggtgt	ccggcatcaa	420
ggccgcctac	gaggccgagc	tcgggggatgc	ccgcaagacc	cttgactcag	tagccaagga	480
gcgcgcccgc	ctgcagctgg	agctgagcaa	agtgcgtgaa	gagtttaagg	agctgaaagc	540
gcgcaatac						549

<210> 168  
 <211> 547  
 <212> DNA  
 <213> Homo sapien

<400> 168

gaattcggca	cgagatggcg	gcagggggtcg	aagcggcggc	ggaggtggcg	gcgacggaga	60
tcaaaatgga	ggaagagagc	ggcgcgcccg	gcgtgccgag	cggcaacggg	gctccggggc	120
ctaagggtga	aggagaacga	cctgctcaga	atgagaagag	gaaggagaaa	aacataaaaa	180
gaggaggcaa	tcgctttgag	ccatatgcc	atccaactaa	aagatacaga	gccttcatta	240
caaacatacc	ttttgatgtg	aaatggcagt	cacttaaaga	cctgggttaa	gaaaaagttg	300
gtgaggtaac	atacgtggag	ctcttaatgg	acgctgaagg	aaagtcaagg	ggatgtgctg	360
ttgttgaatt	caagatggaa	gagagcatga	aaaaagctgc	ggaagtccta	aacaagcata	420
gtctgagcgg	aagaccactg	aaagtcaaag	aagatcctga	tgggtgaacat	gccaggagag	480
caatgcaaaa	ggctggaaga	cttggaagca	cagtatttgt	agcaaactctg	gattataaag	540
ttggctg						547



<210> 169  
 <211> 547  
 <212> DNA  
 <213> Homo sapien

<400> 169  
 gaattcggca ccaggagtcc gactgtgctc gctgctcagc gccgcacccg gaagatgagg 60  
 ctcgccgtgg gagccctgct ggtctgcgcc gtccctggggc tgtgtctggc tgtccctgat 120  
 aaaactgtga gatggtgtgc agtgtcggag catgaggcca ctaagtgcc aagtttccgc 180  
 gaccatatga aaagcgtcat tccatccgat ggtcccagtg ttgcttgtgt gaagaaagcc 240  
 tcctaccttg attgcatcag ggccattgcg gcaaacgaag cggatgctgt gacactggat 300  
 gcaggtttgg tgtatgatgc ttacctggct cccaataacc tgaagcctgt ggtggcagag 360  
 ttctatgggt caaaagagga tccacagact ttctattatg ctgttgctgt ggtgaagaag 420  
 gatagtggct tccagatgaa ccagcttcga ggcaagaagt cctgccacac gggcttaggc 480  
 aggtccgctg ggtggaacat ccccataggc ttactttact gtgacttacc tgagccacgt 540  
 aaacctc 547

<210> 170  
 <211> 838  
 <212> DNA  
 <213> Homo sapien

<400> 170  
 gaattcggca ccagaggagc tcggcctgcg ctgcgccacg atgtccgggg agtcagccag 60  
 gagcttgggg aaggggaagc cgcgcccggg gccggtcccg gagggctcga tccgcattca 120  
 cagcatgagg ttctgcccgt ttgctgagag gacgcgtcta gtcctgaagg ccaagggaat 180  
 caggcatgaa gtcattcaata tcaacctgaa aaataagcct gagtggttct ttaagaaaaa 240  
 tccttttggg ctggtgccag ttctggaaaa cagtcagggt cagctgatct acgagtctgc 300  
 catcacctgt gagtacctgg atgaagcata cccagggaag aagctgttgc cggatgaccc 360  
 ctatgagaaa gcttgccaga agatgatctt agagttgttt tctaagggtg catccttggg 420  
 aggaagcttt attagaagcc aaaataaaga agactatgat ggcctaaaag aagaatttcg 480  
 taaagaattt accaagctag aggaggttct gactaataag aagacgacct tctttggtgg 540  
 caattctatc tctatgattg attacctcat ctggccctgg tttgaacggc tgggaagcaat 600  
 gaagttaaat gagtgtgtag accacactcc aaaactgaaa ctgtggatgg cagccatgaa 660  
 ggaagatccc acagtctcag ccctgcttac tagtgagaaa gactggcaag gtttcctaga 720  
 gctctactta cagaacagcc ctgaggcctg tgactatggg ctctgaaggg ggcaggagtc 780  
 agcaataaag ctatgtctga tattttcctt cactaaaaaa aaaaaaaaaa aactcgag 838

<210> 171  
 <211> 547  
 <212> DNA  
 <213> Homo sapien

<400> 171  
 gaattcggca ccagcgggat ttgggtcgca gttcttgttt gtggattgct gtgatcgtca 60  
 cttgacaatg cagatcttcg tgaagactct gactggtaag accatcaccc tcgagggtga 120  
 gccagtgac accatcgaga atgtcaaggc aaagatccaa gataaggagg gcatccctcc 180  
 tgaccagcag aggtgatct ttgctggaaa acagctggaa gatgggacga ccctgtctga 240  
 ctacaacatc cagaaagagt ccaccctgca cctgggtgct cgtctcagag gtgggatgca 300  
 aatcttcgtg aagacactca ctggcaagac catcacctt gaggtcgagc ccagtgcac 360  
 catcgagaac gtcaaagcaa agatccagga caaggaaggc attcctcctg accagcagag 420  
 gttgatcttt gccggaaagc agctggaaga tgggcgcacc ctgtctgact acaacatcca 480  
 gaaagagtct accctgcacc tgggtgctccg tctcagaggt gggatgcaga tcttcgtgaa 540  
 gaccctg 547



<210> 172  
 <211> 608  
 <212> DNA  
 <213> Homo sapien

<400> 172

gaattcggca	ccagagactt	ctccctctga	ggcctgcgca	ccccctctca	tcagcctgtc	60
caccctcatc	tacaatgggtg	ccctgcccatg	tcagtgcac	cctcaagggtt	caactgagttc	120
tgagtgcac	cctcatgggtg	gtcagtgcct	gtgcaagcct	ggagtgggtg	ggcgccgctg	180
tgacctctgt	gccccctggct	actatggctt	tgccccccaca	ggctgtcaag	gcgcttgcct	240
gggctgccgt	gatcacacag	ggggtgagca	ctgtgaaagg	tgcatgtgtg	gtttccacgg	300
ggacccacgg	ctgccatata	ggggccagtg	ccggccctgt	ccctgtcctg	aaggccctgg	360
gagccaacgg	cacttttgcta	cttcttgcca	ccaggatgaa	tattcccagc	agattgtgtg	420
ccactgccgg	gcaggctata	cggggctgcg	atgtgaagct	tgtgccccctg	ggcactttgg	480
ggacccatca	aggccaggtg	gccggtgcca	actgtgtgag	tgcatgtggga	acattgaccc	540
aatggatcct	gatgcctgtg	acccccacac	ggggcaatgc	ctgcgctgtt	tacaccacac	600
agagggtc						608

<210> 173  
 <211> 543  
 <212> DNA  
 <213> Homo sapien

<400> 173

gaattcggca	ccagagatca	tccgccagca	gggtctggcc	tcctacgact	acgtgcgccc	60
ccgcctcacg	gctgaggacc	tggttcgaggg	tcggatcatc	tctctcgaga	cctacaacct	120
gctccggggag	ggcaccagga	gcctccgtga	ggctctcgag	gcggagtcgg	cctgggtgcta	180
cctctatggc	acgggctccg	tggtctgggtg	ctacctgccc	ggttccaggc	agacactgag	240
catctaccag	gctctcaaga	aagggtctgt	gagtgcggag	gtggccccgccc	tgctgctgga	300
ggcacaggca	gccacaggct	tcctgctgga	cccgggtgaag	ggggaacggc	tgactgtgga	360
tgaagctgtg	cggaaggggc	tcgtggggcc	cgaactgcac	gaccgcctgc	tctcggctga	420
gcggggcggtc	accggctacc	gtgaccacct	caccgagcag	accatctcgc	tcttccaggc	480
catgaagaag	gaactgatcc	ctactgagga	ggccctgcgg	ctgtggatgc	ccagctggcc	540
acc						543

<210> 174  
 <211> 548  
 <212> DNA  
 <213> Homo sapien

<400> 174

gaattcggca	cgagaaatgg	cggcaggggt	cgaagcggcg	gcggagggtg	cggcgacgga	60
gatcaaaatg	gaggaagaga	gcggcgcgcc	cggcgtgccg	agcggcaacg	gggctccggg	120
ccctaagggt	gaaggagaac	gacctgctca	gaatgagaag	aggaaggaga	aaaacataaa	180
aagaggaggc	aatcgctttg	agccatatgc	caatccaact	aaaagataca	gagccttcat	240
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tagtctgagc	ggaagaccac	tgaaagtcaa	agaagatcct	gatgggtgaac	atgccaggag	480
agcaatgcaa	aagggtgatgg	ctacgactgg	tgggatgggt	atgggaccag	gtggcccagg	540
aatgatta						548

<210> 175  
 <211> 604  
 <212> DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 175

gaattcggca	ccagaggacc	tccaggacat	gttcacgcgc	cataccatcg	aggagattga	60
gggcctgac	tcagcccatg	accagttcaa	gtccaccctg	ccggacgccg	atagggagcg	120
cgaggccatc	ctggccatcc	acaaggaggc	ccagaggatc	gctgagagca	accacatcaa	180
gctgtcgggc	agcaaccctt	acaccaccgt	caccccgcaa	atcatcaact	ccaagtggga	240
gaaggtgcag	cagctggtgc	caaaacggga	ccatgccctc	ctggaggagc	agagcaagca	300
gcagtccaac	gagcacctgc	gccgccagtt	cgccagccag	gccaatgttg	tggggccctg	360
gatccagacc	aagatggagg	agatcgggcg	catctccatt	gagatgaacg	ggaccctgga	420
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ggacctgctg	gagcagcagc	accagcttat	ccaggaggcc	ctcatcttcg	acaacaagca	540
caccaactat	accatggagc	acatccgcgt	gggctgggag	cagctgctca	ccaccattgc	600
ccgg						604

&lt;210&gt; 176

&lt;211&gt; 486

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 176

gaattcggca	ccagccaagc	tcactattga	atccacgccg	ttcaatgtcg	cagaggggaa	60
ggaggttctt	ctactcgccc	acaacctgcc	ccagaatcgt	attgggtaca	gctgggtacaa	120
aggcgaaaga	gtggatggca	acagtcta	tgtaggatat	gtaataggaa	ctcaacaagc	180
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ctccagcaac	aactccaacc	ccgtggagga	caaggatgct	gtggccttca	cctgtgaacc	420
tgaggttcag	aacacaacct	acctgtggtg	ggtaaattggt	cagagcctcc	cggtcagtcc	480
caaggc						486

&lt;210&gt; 177

&lt;211&gt; 387

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 177

gaattcggca	ccagggacag	cagaccagac	agtcacagca	gccttgacaa	aacgttcctg	60
gaactcaagc	tcttctccac	agaggaggac	agagcagaca	gcagagacca	tggagtctcc	120
ctcggccctt	ccccacagat	ggtgcatccc	ctggcagagg	ctcctgctca	cagcctcact	180
tctaaccctt	tggaaccctg	ccaccactgc	caagctcact	attgaatcca	cgccgttcaa	240
tgctgcagag	gggaaggagg	tgcttctact	tgtccacaat	ctgccccagc	atcttttttg	300
ctacagctgg	tacaaagggtg	aaagagtggg	tggcaaccgt	caaattatag	gatatgtaat	360
aggaactcaa	caagctaccc	cagggcc				387

&lt;210&gt; 178

&lt;211&gt; 440

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 178

gaattcggca	cgaggagaag	cagaaaaaca	aggaatttag	ccagacttta	gaaaatgaga	60
aaaatacctt	actgagtcag	atatcaacaa	aggatggtga	actaaaaatg	cttcaggagg	120
aagtaaccaa	aatgaacctg	ttaaatcagc	aaatccaaga	agaactctct	agagttacca	180
aactaaagga	gacagcagaa	gaagagaaag	atgatttgga	agagaggctt	atgaatcaat	240

tagcagaact	taatggaagc	attgggaatt	actgtcagga	tgttacagat	gcccaaataa	300
aaaatgagct	attggaatct	gaaatgaaga	accttaaaaa	gtgtgtgagt	gaattggaag	360
aagaaaagca	gcagttagtc	aaggaaaaaa	ctaagggtgga	atcagaaata	cgaaaggaat	420
atttggagaa	aatacaaggt					440

<210> 179  
 <211> 443  
 <212> DNA  
 <213> Homo sapien

<400> 179						
gaattcggca	ccagcggggg	gctacggcgg	cggctacggc	ggcgtcctga	ccgcgtccga	60
cgggctgctg	gcgggcaacg	agaagctaac	catgcagaac	ctcaacgacc	gcctggcctc	120
ctacctggac	aaggtgcgcg	ccctggaggc	ggccaacggc	gagctagagg	tgaagatccg	180
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gcagatcgac	aacgcccgtc	tggctgcaga	tgacttccga	accaagtttg	agacgggaca	360
ggctctgcgc	atgagcgtgg	aggccgacat	caacggcctg	cgcaggggtgc	tggatgagct	420
gaccctggcc	aggaccgacc	tgg				443

<210> 180  
 <211> 403  
 <212> DNA  
 <213> Homo sapien

<400> 180						
gaattcggca	cgagggttatg	agagtcgact	tcaatgttcc	tatgaagaac	aaccagataa	60
caaacaacca	gaggattaag	gctgctgtcc	caagcatcaa	attctgcttg	gacaatggag	120
ccaagtcggg	agtccttatg	agccacctag	gccggcctga	tggtgtgccc	atgcctgaca	180
agtactcctt	agagccagtt	gctgtagaac	tcagatctct	gctggggcaag	gatgttctgt	240
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ctgtcatcct	gctggagaac	ctccgctttc	atgtggagga	agaagggaag	ggaaaagatg	360
cttctgggaa	caagggttaa	gccgagccag	ccaaaataga	agc		403

<210> 181  
 <211> 493  
 <212> DNA  
 <213> Homo sapien

<400> 181						
gaattcggca	ccagcagagg	tctccagagc	cttctctctc	ctgtgcaaaa	tggcaactct	60
taaggaaaaa	ctcattgcac	cagttgcgga	agaagaggca	acagttccaa	acaataagat	120
cactgtagtg	ggtgttggac	aagttggtat	ggcgtgtgct	atcagcattc	tgggaaagtc	180
tctggctgat	gaacttgctc	ttgtggatgt	tttggaagat	aagcttaaag	gagaaatgat	240
ggatctgcag	catgggagct	tatttcttca	gacacctaaa	attgtggcag	ataaagatta	300
ttctgtgacc	gccaattcta	agattgtagt	ggtaactgca	ggagtccgtc	agcaagaagg	360
ggagagtcgg	ctcaatctgg	tgagagaaaa	tgttaatgtc	ttcaaattca	ttattcctca	420
gatcgtcaag	tacagtcctg	attgcatcat	aattgtgggt	tccaacccag	tggacattct	480
tacgtatggt	acc					493

<210> 182  
 <211> 209  
 <212> PRT  
 <213> Homo sapien

<400> 182

Ala	Phe	Ser	Ser	Asn	Pro	Lys	Val	Gln	Val	Glu	Ala	Ile	Glu	Gly	Gly
1				5					10					15	
Ala	Leu	Gln	Lys	Leu	Leu	Val	Ile	Leu	Ala	Thr	Glu	Gln	Pro	Leu	Thr
			20					25					30		
Ala	Lys	Lys	Lys	Val	Leu	Phe	Ala	Leu	Cys	Ser	Leu	Leu	Arg	His	Phe
		35					40					45			
Pro	Tyr	Ala	Gln	Arg	Gln	Phe	Leu	Lys	Leu	Gly	Gly	Leu	Gln	Val	Leu
	50					55					60				
Arg	Thr	Leu	Val	Gln	Glu	Lys	Gly	Thr	Glu	Val	Leu	Ala	Val	Arg	Val
65					70					75					80
Val	Thr	Leu	Leu	Tyr	Asp	Leu	Val	Thr	Glu	Lys	Met	Phe	Ala	Glu	Glu
				85					90					95	
Glu	Ala	Glu	Leu	Thr	Gln	Glu	Met	Ser	Pro	Glu	Lys	Leu	Gln	Gln	Tyr
			100					105					110		
Arg	Gln	Val	His	Leu	Leu	Pro	Gly	Leu	Trp	Glu	Gln	Gly	Trp	Cys	Glu
		115					120					125			
Ile	Thr	Ala	His	Leu	Leu	Ala	Leu	Pro	Glu	His	Asp	Ala	Arg	Glu	Lys
	130					135					140				
Val	Leu	Gln	Thr	Leu	Gly	Val	Leu	Leu	Thr	Thr	Cys	Arg	Asp	Arg	Tyr
145					150					155					160
Arg	Gln	Asp	Pro	Gln	Leu	Gly	Arg	Thr	Leu	Ala	Ser	Leu	Gln	Ala	Glu
				165					170					175	
Tyr	Gln	Val	Leu	Ala	Ser	Leu	Glu	Leu	Gln	Asp	Gly	Glu	Asp	Glu	Gly
			180				185					190			
Tyr	Phe	Gln	Glu	Leu	Leu	Gly	Ser	Val	Asn	Ser	Leu	Leu	Lys	Glu	Leu
		195					200					205			

Arg

<210> 183  
 <211> 255  
 <212> PRT  
 <213> Homo sapien

<400> 183

Met	Ala	Ala	Gly	Val	Glu	Ala	Ala	Ala	Glu	Val	Ala	Ala	Thr	Glu	Pro
1				5					10					15	
Lys	Met	Glu	Glu	Glu	Ser	Gly	Ala	Pro	Cys	Val	Pro	Ser	Gly	Asn	Gly
			20					25					30		
Ala	Pro	Gly	Pro	Lys	Gly	Glu	Glu	Arg	Pro	Thr	Gln	Asn	Glu	Lys	Arg
		35					40					45			
Lys	Glu	Lys	Asn	Ile	Lys	Arg	Gly	Gly	Asn	Arg	Phe	Glu	Pro	Tyr	Ser
	50					55					60				
Asn	Pro	Thr	Lys	Arg	Tyr	Arg	Ala	Phe	Ile	Thr	Asn	Ile	Pro	Phe	Asp
65					70					75					80
Val	Lys	Trp	Gln	Ser	Leu	Lys	Asp	Leu	Val	Lys	Glu	Lys	Val	Gly	Glu
				85					90					95	
Val	Thr	Tyr	Val	Glu	Leu	Leu	Met	Asp	Ala	Glu	Gly	Lys	Ser	Arg	Gly
			100					105					110		
Cys	Ala	Val	Val	Glu	Phe	Lys	Met	Glu	Glu	Ser	Met	Lys	Lys	Ala	Ala
		115					120					125			
Glu	Val	Leu	Asn	Lys	His	Ser	Leu	Ser	Gly	Arg	Pro	Leu	Lys	Val	Lys
	130					135					140				
Glu	Asp	Pro	Asp	Gly	Glu	His	Ala	Arg	Arg	Ala	Met	Gln	Lys	Ala	Gly

80

145		150		155		160									
Arg	Leu	Gly	Ser	Thr	Val	Phe	Val	Ala	Asn	Leu	Asp	Tyr	Lys	Val	Gly
				165					170					175	
Trp	Lys	Lys	Leu	Lys	Glu	Val	Phe	Ser	Met	Ala	Gly	Val	Val	Val	Arg
			180					185					190		
Ala	Asp	Ile	Leu	Glu	Asp	Lys	Asp	Gly	Lys	Ser	Arg	Gly	Ile	Gly	Ile
		195				200					205				
Val	Thr	Phe	Glu	Gln	Ser	Ile	Glu	Ala	Val	Gln	Ala	Ile	Ser	Met	Phe
	210					215				220					
Asn	Gly	Gln	Leu	Leu	Phe	Asp	Arg	Pro	Met	His	Val	Lys	Met	Asp	Glu
225					230					235				240	
Arg	Ala	Leu	Pro	Lys	Gly	Asp	Phe	Phe	Pro	Pro	Glu	Arg	His	Ser	
			245						250					255	

<210> 184  
 <211> 188  
 <212> PRT  
 <213> Homo sapien

<400> 184
Leu Ser Gly Ser Cys Ile Arg Arg Glu Gln Thr Pro Glu Lys Glu Lys
1 5 10 15
Gln Val Val Leu Phe Glu Glu Ala Ser Trp Thr Cys Thr Pro Ala Cys
20 25 30
Gly Asp Glu Pro Arg Thr Val Ile Leu Leu Ser Ser Met Leu Ala Asp
35 40 45
His Arg Leu Lys Leu Glu Asp Tyr Lys Asp Arg Leu Lys Ser Gly Glu
50 55 60
His Leu Asn Pro Asp Gln Leu Glu Ala Val Glu Lys Tyr Glu Glu Val
65 70 75 80
Leu His Asn Leu Glu Phe Ala Lys Glu Leu Gln Lys Thr Phe Ser Gly
85 90 95
Leu Ser Leu Asp Leu Leu Lys Ala Gln Lys Lys Ala Gln Arg Arg Glu
100 105 110
His Met Leu Lys Leu Glu Ala Glu Lys Lys Lys Leu Arg Thr Ile Leu
115 120 125
Gln Val Gln Tyr Val Leu Gln Asn Leu Thr Gln Glu His Val Gln Lys
130 135 140
Asp Phe Lys Gly Gly Leu Asn Gly Ala Val Tyr Leu Pro Ser Lys Glu
145 150 155 160
Leu Asp Tyr Leu Ile Lys Phe Ser Lys Leu Thr Cys Pro Glu Arg Asn
165 170 175
Glu Ser Leu Arg Gln Thr Leu Glu Gly Ser Thr Val
180 185

<210> 185  
 <211> 746  
 <212> PRT  
 <213> Homo sapien

<400> 185
Asp Lys His Leu Lys Asp Leu Leu Ser Lys Leu Leu Asn Ser Gly Tyr
1 5 10 15
Phe Glu Ser Ile Pro Val Pro Lys Asn Ala Lys Glu Lys Glu Val Pro
20 25 30

Leu	Glu	Glu	Glu	Met	Leu	Ile	Gln	Ser	Glu	Lys	Lys	Thr	Gln	Leu	Ser
	35						40					45			
Lys	Thr	Glu	Ser	Val	Lys	Glu	Ser	Glu	Ser	Leu	Met	Glu	Phe	Ala	Gln
	50					55					60				
Pro	Glu	Ile	Gln	Pro	Gln	Glu	Phe	Leu	Asn	Arg	Arg	Tyr	Met	Thr	Glu
65					70				75						80
Val	Asp	Tyr	Ser	Asn	Lys	Gln	Gly	Glu	Glu	Gln	Pro	Trp	Glu	Ala	Asp
				85					90					95	
Tyr	Ala	Arg	Lys	Pro	Asn	Leu	Pro	Lys	Arg	Trp	Asp	Met	Leu	Thr	Glu
			100					105					110		
Pro	Asp	Gly	Gln	Glu	Lys	Lys	Gln	Glu	Ser	Phe	Lys	Ser	Trp	Glu	Ala
		115					120					125			
Ser	Gly	Lys	His	Gln	Glu	Val	Ser	Lys	Pro	Ala	Val	Ser	Leu	Glu	Gln
	130					135					140				
Arg	Lys	Gln	Asp	Thr	Ser	Lys	Leu	Arg	Ser	Thr	Leu	Pro	Glu	Glu	Gln
145					150					155					160
Lys	Lys	Gln	Glu	Ile	Ser	Lys	Ser	Lys	Pro	Ser	Pro	Ser	Gln	Trp	Lys
				165					170					175	
Gln	Asp	Thr	Pro	Lys	Ser	Lys	Ala	Gly	Tyr	Val	Gln	Glu	Glu	Gln	Lys
			180					185					190		
Lys	Gln	Glu	Thr	Pro	Lys	Leu	Trp	Pro	Val	Gln	Leu	Gln	Lys	Glu	Gln
		195					200					205			
Asp	Pro	Lys	Lys	Gln	Thr	Pro	Lys	Ser	Trp	Thr	Pro	Ser	Met	Gln	Ser
	210					215					220				
Glu	Gln	Asn	Thr	Thr	Lys	Ser	Trp	Thr	Thr	Pro	Met	Cys	Glu	Glu	Gln
225					230					235					240
Asp	Ser	Lys	Gln	Pro	Glu	Thr	Pro	Lys	Ser	Trp	Glu	Asn	Asn	Val	Glu
				245					250					255	
Ser	Gln	Lys	His	Ser	Leu	Thr	Ser	Gln	Ser	Gln	Ile	Ser	Pro	Lys	Ser
			260					265					270		
Trp	Gly	Val	Ala	Thr	Ala	Ser	Leu	Ile	Pro	Asn	Asp	Gln	Leu	Leu	Pro
		275					280					285			
Arg	Lys	Leu	Asn	Thr	Glu	Pro	Lys	Asp	Val	Pro	Lys	Pro	Val	His	Gln
	290					295					300				
Pro	Val	Gly	Ser	Ser	Ser	Thr	Leu	Pro	Lys	Asp	Pro	Val	Leu	Arg	Lys
305					310					315					320
Glu	Lys	Leu	Gln	Asp	Leu	Met	Thr	Gln	Ile	Gln	Gly	Thr	Cys	Asn	Phe
				325					330					335	
Met	Gln	Glu	Ser	Val	Leu	Asp	Phe	Asp	Lys	Pro	Ser	Ser	Ala	Ile	Pro
				340				345					350		
Thr	Ser	Gln	Pro	Pro	Ser	Ala	Thr	Pro	Gly	Ser	Pro	Val	Ala	Ser	Lys
		355					360					365			
Glu	Gln	Asn	Leu	Ser	Ser	Gln	Ser	Asp	Phe	Leu	Gln	Glu	Pro	Leu	Gln
		370				375					380				
Val	Phe	Asn	Val	Asn	Ala	Pro	Leu	Pro	Pro	Arg	Lys	Glu	Gln	Glu	Ile
385					390					395					400
Lys	Glu	Ser	Pro	Tyr	Ser	Pro	Gly	Tyr	Asn	Gln	Ser	Phe	Thr	Thr	Ala
				405					410					415	
Ser	Thr	Gln	Thr	Pro	Pro	Gln	Cys	Gln	Leu	Pro	Ser	Ile	His	Val	Glu
			420					425				430			
Gln	Thr	Val	His	Ser	Gln	Glu	Thr	Ala	Ala	Asn	Tyr	His	Pro	Asp	Gly
		435					440					445			
Thr	Ile	Gln	Val	Ser	Asn	Gly	Ser	Leu	Ala	Phe	Tyr	Pro	Ala	Gln	Thr
	450					455					460				
Asn	Val	Phe	Pro	Arg	Pro	Thr	Gln	Pro	Phe	Val	Asn	Ser	Arg	Gly	Ser



465					470					475				480	
Val	Arg	Gly	Cys	Thr	Arg	Gly	Gly	Arg	Leu	Ile	Thr	Asn	Ser	Tyr	Arg
				485					490					495	
Ser	Pro	Gly	Gly	Tyr	Lys	Gly	Phe	Asp	Thr	Tyr	Arg	Gly	Leu	Pro	Ser
			500					505					510		
Ile	Ser	Asn	Gly	Asn	Tyr	Ser	Gln	Leu	Gln	Phe	Gln	Ala	Arg	Glu	Tyr
		515					520					525			
Ser	Gly	Ala	Pro	Tyr	Ser	Gln	Arg	Asp	Asn	Phe	Gln	Gln	Cys	Tyr	Lys
	530					535					540				
Arg	Gly	Gly	Thr	Ser	Gly	Gly	Pro	Arg	Ala	Asn	Ser	Arg	Ala	Gly	Trp
545					550					555					560
Ser	Asp	Ser	Ser	Gln	Val	Ser	Ser	Pro	Glu	Arg	Asp	Asn	Glu	Thr	Phe
				565					570					575	
Asn	Ser	Gly	Asp	Ser	Gly	Gln	Gly	Asp	Ser	Arg	Ser	Met	Thr	Pro	Val
			580					585					590		
Asp	Val	Pro	Val	Thr	Asn	Pro	Ala	Ala	Thr	Ile	Leu	Pro	Val	His	Val
	595						600					605			
Tyr	Pro	Leu	Pro	Gln	Gln	Met	Arg	Val	Ala	Phe	Ser	Ala	Ala	Arg	Thr
	610					615					620				
Ser	Asn	Leu	Ala	Pro	Gly	Thr	Leu	Asp	Gln	Pro	Ile	Val	Phe	Asp	Leu
625					630					635					640
Leu	Leu	Asn	Asn	Leu	Gly	Glu	Thr	Phe	Asp	Leu	Gln	Leu	Gly	Arg	Phe
				645					650					655	
Asn	Cys	Pro	Val	Asn	Gly	Thr	Tyr	Val	Phe	Ile	Phe	His	Met	Leu	Lys
			660					665					670		
Leu	Ala	Val	Asn	Val	Pro	Leu	Tyr	Val	Asn	Leu	Met	Lys	Asn	Glu	Glu
	675						680					685			
Val	Leu	Val	Ser	Ala	Tyr	Ala	Asn	Asp	Gly	Ala	Pro	Asp	His	Glu	Thr
	690					695						700			
Ala	Ser	Asn	His	Ala	Ile	Leu	Gln	Leu	Phe	Gln	Gly	Asp	Gln	Ile	Trp
705					710					715					720
Leu	Arg	Leu	His	Arg	Gly	Ala	Ile	Tyr	Gly	Ser	Ser	Trp	Lys	Tyr	Ser
				725					730					735	
Thr	Phe	Ser	Gly	Tyr	Leu	Leu	Tyr	Gln	Asp						
			740					745							

&lt;210&gt; 186

&lt;211&gt; 705

&lt;212&gt; PRT

&lt;213&gt; Homo sapien

&lt;400&gt; 186

Ala	Leu	Leu	Asn	Val	Arg	Gln	Pro	Pro	Ser	Thr	Thr	Thr	Phe	Val	Leu
1				5					10					15	
Asn	Gln	Ile	Asn	His	Leu	Pro	Pro	Leu	Gly	Ser	Thr	Ile	Val	Met	Thr
			20					25					30		
Lys	Thr	Pro	Pro	Val	Thr	Thr	Asn	Arg	Gln	Thr	Ile	Thr	Leu	Thr	Lys
	35						40					45			
Phe	Ile	Gln	Thr	Thr	Ala	Ser	Thr	Arg	Pro	Ser	Val	Ser	Ala	Pro	Thr
	50					55					60				
Val	Arg	Asn	Ala	Met	Thr	Ser	Ala	Pro	Ser	Lys	Asp	Gln	Val	Gln	Leu
65					70					75					80
Lys	Asp	Leu	Leu	Lys	Asn	Asn	Ser	Leu	Asn	Glu	Leu	Met	Lys	Leu	Lys
				85					90					95	
Pro	Pro	Ala	Asn	Ile	Ala	Gln	Pro	Val	Ala	Thr	Ala	Ala	Thr	Asp	Val

			100					105				110				
Ser	Asn	Gly	Thr	Val	Lys	Lys	Glu	Ser	Ser	Asn	Lys	Glu	Gly	Ala	Arg	
		115					120					125				
Met	Trp	Ile	Asn	Asp	Met	Lys	Met	Arg	Ser	Phe	Ser	Pro	Thr	Met	Lys	
	130					135					140					
Val	Pro	Val	Val	Lys	Glu	Asp	Asp	Glu	Pro	Glu	Glu	Glu	Asp	Glu	Glu	
145					150					155					160	
Glu	Met	Gly	His	Ala	Glu	Thr	Tyr	Ala	Glu	Tyr	Met	Pro	Ile	Lys	Leu	
			165						170					175		
Lys	Ile	Gly	Leu	Arg	His	Pro	Asp	Ala	Val	Val	Glu	Thr	Ser	Ser	Leu	
		180					185					190				
Ser	Ser	Val	Thr	Pro	Pro	Asp	Val	Trp	Tyr	Lys	Thr	Ser	Ile	Ser	Glu	
	195						200					205				
Glu	Thr	Ile	Asp	Asn	Gly	Trp	Leu	Ser	Ala	Leu	Gln	Leu	Glu	Ala	Ile	
	210					215					220					
Thr	Tyr	Ala	Ala	Gln	Gln	His	Glu	Thr	Phe	Leu	Pro	Asn	Gly	Asp	Arg	
225				230					235						240	
Ala	Gly	Phe	Leu	Ile	Gly	Asp	Gly	Ala	Gly	Val	Gly	Lys	Gly	Arg	Thr	
			245						250					255		
Ile	Ala	Gly	Ile	Ile	Tyr	Glu	Asn	Tyr	Leu	Leu	Ser	Arg	Lys	Arg	Ala	
		260					265					270				
Leu	Trp	Phe	Ser	Val	Ser	Asn	Asp	Leu	Lys	Tyr	Asp	Ala	Glu	Arg	Asp	
	275						280					285				
Leu	Arg	Asp	Ile	Gly	Ala	Lys	Asn	Ile	Leu	Val	His	Ser	Leu	Asn	Lys	
	290					295					300					
Phe	Lys	Tyr	Gly	Lys	Ile	Ser	Ser	Lys	His	Asn	Gly	Ser	Val	Lys	Lys	
305				310						315					320	
Gly	Val	Ile	Phe	Ala	Thr	Tyr	Ser	Ser	Leu	Ile	Gly	Glu	Ser	Gln	Ser	
			325						330					335		
Gly	Gly	Lys	Tyr	Lys	Thr	Arg	Leu	Lys	Gln	Leu	Leu	His	Trp	Cys	Gly	
		340						345				350				
Asp	Asp	Phe	Asp	Gly	Val	Ile	Val	Phe	Asp	Glu	Cys	His	Lys	Ala	Lys	
	355						360					365				
Asn	Leu	Cys	Pro	Val	Gly	Ser	Ser	Lys	Pro	Thr	Lys	Thr	Gly	Leu	Ala	
	370					375					380					
Val	Leu	Glu	Leu	Gln	Asn	Lys	Leu	Pro	Lys	Ala	Arg	Val	Val	Tyr	Ala	
385				390						395					400	
Ser	Ala	Thr	Gly	Ala	Ser	Glu	Pro	Arg	Asn	Met	Ala	Tyr	Met	Asn	Arg	
			405						410					415		
Leu	Gly	Ile	Trp	Gly	Glu	Gly	Thr	Pro	Phe	Arg	Glu	Phe	Ser	Asp	Phe	
		420					425					430				
Ile	Gln	Ala	Val	Glu	Arg	Arg	Gly	Val	Gly	Ala	Met	Glu	Ile	Val	Ala	
	435						440					445				
Met	Asp	Met	Lys	Leu	Arg	Gly	Met	Tyr	Ile	Ala	Arg	Gln	Leu	Ser	Phe	
	450					455					460					
Thr	Gly	Val	Thr	Phe	Lys	Ile	Glu	Glu	Val	Leu	Leu	Ser	Gln	Ser	Tyr	
465				470						475					480	
Val	Lys	Met	Tyr	Asn	Lys	Ala	Val	Lys	Leu	Trp	Val	Ile	Ala	Arg	Glu	
			485						490					495		
Arg	Phe	Gln	Gln	Ala	Ala	Asp	Leu	Ile	Asp	Ala	Glu	Gln	Arg	Met	Lys	
		500						505				510				
Lys	Ser	Met	Trp	Gly	Gln	Phe	Trp	Ser	Ala	His	Gln	Arg	Phe	Phe	Lys	
	515						520					525				
Tyr	Leu	Cys	Ile	Ala	Ser	Lys	Val	Lys	Arg	Val	Val	Gln	Leu	Ala	Arg	
	530					535					540					

Glu Glu Ile Lys Asn Gly Lys Cys Val Val Ile Gly Leu Gln Ser Thr  
 545 550 555 560  
 Gly Glu Ala Arg Thr Leu Glu Ala Leu Glu Gly Gly Gly Glu Leu  
 565 570 575  
 Asn Asp Phe Val Ser Thr Ala Lys Gly Val Leu Gln Ser Leu Ile Glu  
 580 585 590  
 Lys His Phe Pro Ala Pro Asp Arg Lys Lys Leu Tyr Ser Leu Leu Gly  
 595 600 605  
 Ile Asp Leu Thr Ala Pro Ser Asn Asn Ser Ser Pro Arg Asp Ser Pro  
 610 615 620  
 Cys Lys Glu Asn Lys Ile Lys Lys Arg Lys Gly Glu Glu Ile Thr Arg  
 625 630 635 640  
 Glu Ala Lys Lys Ala Arg Lys Val Gly Gly Leu Thr Gly Ser Ser Ser  
 645 650 655  
 Asp Asp Ser Gly Ser Glu Ser Asp Ala Ser Asp Asn Glu Glu Ser Asp  
 660 665 670  
 Tyr Glu Ser Ser Lys Asn Met Ser Ser Gly Asp Asp Asp Asp Phe Asn  
 675 680 685  
 Pro Phe Leu Asp Glu Ser Asn Glu Asp Asp Glu Asn Asp Pro Trp Leu  
 690 695 700  
 Ile  
 705

<210> 187  
 <211> 595  
 <212> PRT  
 <213> Homo sapien

<400> 187  
 Glu Ser Pro Arg His Arg Gly Glu Gly Gly Gly Glu Trp Gly Pro Gly  
 1 5 10 15  
 Val Pro Arg Glu Arg Arg Glu Ser Ala Gly Glu Trp Gly Ala Asp Thr  
 20 25 30  
 Pro Lys Glu Gly Gly Glu Ser Ala Gly Glu Trp Gly Ala Glu Val Pro  
 35 40 45  
 Arg Gly Arg Gly Glu Gly Ala Gly Glu Trp Gly Pro Asp Thr Pro Lys  
 50 55 60  
 Glu Arg Gly Gln Gly Val Arg Glu Trp Gly Pro Glu Ile Pro Gln Glu  
 65 70 75 80  
 His Gly Glu Ala Thr Arg Asp Trp Ala Leu Glu Ser Pro Arg Ala Leu  
 85 90 95  
 Gly Glu Asp Ala Arg Glu Leu Gly Ser Ser Pro His Asp Arg Gly Ala  
 100 105 110  
 Ser Pro Arg Asp Leu Ser Gly Glu Ser Pro Cys Thr Gln Arg Ser Gly  
 115 120 125  
 Leu Leu Pro Glu Arg Arg Gly Asp Ser Pro Trp Pro Pro Trp Pro Ser  
 130 135 140  
 Pro Gln Glu Arg Asp Ala Gly Thr Arg Asp Arg Glu Glu Ser Pro Arg  
 145 150 155 160  
 Asp Trp Gly Gly Ala Glu Ser Pro Arg Gly Trp Glu Ala Gly Pro Arg  
 165 170 175  
 Glu Trp Gly Pro Ser Pro Ser Gly His Gly Asp Gly Pro Arg Arg Arg  
 180 185 190  
 Pro Arg Lys Arg Arg Gly Arg Lys Gly Arg Met Gly Arg Gln His Glu  
 195 200 205

Ala	Ala	Ala	Thr	Ala	Ala	Thr	Ala	Ala	Thr	Ala	Thr	Gly	Gly	Thr	Ala
210						215						220			
Glu	Glu	Ala	Gly	Ala	Ser	Ala	Pro	Glu	Ser	Gln	Ala	Gly	Gly	Gly	Pro
225					230					235					240
Arg	Gly	Arg	Ala	Arg	Gly	Pro	Arg	Gln	Gln	Gly	Arg	Arg	Arg	His	Gly
				245					250					255	
Thr	Gln	Arg	Arg	Arg	Gly	Pro	Pro	Gln	Ala	Arg	Glu	Glu	Gly	Pro	Arg
			260					265					270		
Asp	Ala	Thr	Thr	Ile	Leu	Gly	Leu	Gly	Thr	Pro	Ser	Gly	Glu	Gln	Arg
	275						280					285			
Ala	Asp	Gln	Ser	Gln	Ala	Leu	Pro	Ala	Leu	Ala	Gly	Ala	Ala	Ala	Ala
290						295					300				
His	Ala	His	Ala	Ile	Pro	Gly	Ala	Gly	Pro	Ala	Ala	Ala	Pro	Val	Gly
305					310					315					320
Gly	Arg	Gly	Arg	Arg	Gly	Gly	Trp	Arg	Gly	Gly	Arg	Arg	Gly	Gly	Ser
				325					330					335	
Ala	Gly	Ala	Gly	Gly	Gly	Gly	Arg	Gly	Gly	Arg	Gly	Arg	Gly	Arg	Gly
			340					345					350		
Gly	Gly	Arg	Gly	Gly	Gly	Gly	Ala	Gly	Arg	Gly	Gly	Gly	Ala	Ala	Gly
		355					360					365			
Pro	Arg	Glu	Gly	Ala	Ser	Ser	Pro	Gly	Ala	Arg	Arg	Gly	Glu	Gln	Arg
370						375					380				
Arg	Arg	Gly	Arg	Gly	Pro	Pro	Ala	Ala	Gly	Ala	Ala	Gln	Val	Ser	Ala
385					390					395					400
Arg	Gly	Arg	Arg	Ala	Arg	Gly	Gln	Arg	Ala	Gly	Glu	Glu	Ala	Gln	Asp
				405					410					415	
Gly	Leu	Leu	Pro	Arg	Gly	Arg	Asp	Arg	Leu	Pro	Leu	Arg	Pro	Gly	Asp
			420				425					430			
Ala	Asn	Gln	Arg	Ala	Glu	Arg	Pro	Gly	Pro	Pro	Arg	Gly	Gly	His	Gly
	435						440					445			
Pro	Val	Asn	Ala	Ser	Ser	Ala	Pro	Asp	Thr	Ser	Pro	Pro	Arg	His	Pro
450						455					460				
Arg	Arg	Trp	Val	Ser	Gln	Gln	Arg	Gln	Arg	Leu	Trp	Arg	Gln	Phe	Arg
465					470					475					480
Val	Gly	Gly	Gly	Phe	Pro	Pro	Pro	Pro	Pro	Ser	Arg	Pro	Pro	Ala	Val
				485					490					495	
Leu	Leu	Pro	Leu	Leu	Arg	Leu	Ala	Cys	Ala	Gly	Asp	Pro	Gly	Ala	Thr
			500				505						510		
Arg	Pro	Gly	Pro	Arg	Arg	Pro	Ala	Arg	Arg	Pro	Arg	Gly	Glu	Leu	Ile
		515					520					525			
Pro	Arg	Arg	Pro	Asp	Pro	Ala	Ala	Pro	Ser	Glu	Glu	Gly	Leu	Arg	Met
530						535					540				
Glu	Ser	Ser	Val	Asp	Asp	Gly	Ala	Thr	Ala	Thr	Thr	Ala	Asp	Ala	Ala
545					550					555					560
Ser	Gly	Glu	Ala	Pro	Glu	Ala	Gly	Pro	Ser	Pro	Ser	His	Ser	Pro	Thr
				565					570					575	
Met	Cys	Gln	Thr	Gly	Gly	Pro	Gly	Pro	Pro	Pro	Pro	Gln	Pro	Pro	Arg
			580					585					590		
Trp	Leu	Pro													
		595													

&lt;210&gt; 188

&lt;211&gt; 376

&lt;212&gt; PRT

&lt;213&gt; Homo sapien

<400> 188  
 Glu Met Arg Lys Phe Asp Val Pro Ser Met Glu Ser Thr Leu Asn Gln  
 1 5 10 15  
 Pro Ala Met Leu Glu Thr Leu Tyr Ser Asp Pro His Tyr Arg Ala His  
 20 25 30  
 Phe Pro Asn Pro Arg Pro Asp Thr Asn Lys Asp Val Tyr Lys Val Leu  
 35 40 45  
 Pro Glu Ser Lys Lys Ala Pro Gly Ser Gly Ala Val Phe Glu Arg Asn  
 50 55 60  
 Gly Pro His Ala Ser Ser Ser Gly Val Leu Pro Leu Gly Leu Gln Pro  
 65 70 75 80  
 Ala Pro Gly Leu Ser Lys Ser Leu Ser Ser Gln Val Trp Gln Pro Ser  
 85 90 95  
 Pro Asp Pro Trp His Pro Gly Glu Gln Ser Cys Glu Leu Ser Thr Cys  
 100 105 110  
 Arg Gln Gln Leu Glu Leu Ile Arg Leu Gln Met Glu Gln Met Gln Leu  
 115 120 125  
 Gln Asn Gly Ala Met Cys His His Pro Ala Ala Phe Ala Pro Leu Leu  
 130 135 140  
 Pro Thr Leu Glu Pro Ala Gln Trp Leu Ser Ile Leu Asn Ser Asn Glu  
 145 150 155 160  
 His Leu Leu Lys Glu Lys Glu Leu Leu Ile Asp Lys Gln Arg Lys His  
 165 170 175  
 Ile Ser Gln Leu Glu Gln Lys Val Arg Glu Ser Glu Leu Gln Val His  
 180 185 190  
 Ser Ala Leu Leu Gly Arg Pro Ala Pro Phe Gly Asp Val Cys Leu Leu  
 195 200 205  
 Arg Leu Gln Glu Leu Gln Arg Glu Asn Thr Phe Leu Arg Ala Gln Phe  
 210 215 220  
 Ala Gln Lys Thr Glu Ala Leu Ser Lys Glu Lys Met Glu Leu Glu Lys  
 225 230 235 240  
 Lys Leu Ser Ala Ser Glu Val Glu Ile Gln Leu Ile Arg Glu Ser Leu  
 245 250 255  
 Lys Val Thr Leu Gln Lys His Ser Glu Glu Gly Lys Lys Gln Glu Glu  
 260 265 270  
 Arg Val Lys Gly Arg Asp Lys His Ile Asn Asn Leu Lys Lys Lys Cys  
 275 280 285  
 Gln Lys Glu Ser Glu Gln Asn Arg Glu Lys Gln Gln Arg Ile Glu Thr  
 290 295 300  
 Leu Glu Arg Tyr Leu Ala Asp Leu Pro Thr Leu Glu Asp His Gln Lys  
 305 310 315 320  
 Gln Thr Glu Gln Leu Lys Asp Ala Glu Leu Lys Asn Thr Glu Leu Gln  
 325 330 335  
 Glu Arg Val Ala Glu Leu Glu Thr Leu Leu Glu Asp Thr Gln Ala Thr  
 340 345 350  
 Cys Arg Glu Lys Glu Val Gln Leu Glu Ser Leu Arg Gln Arg Glu Ala  
 355 360 365  
 Asp Leu Ser Ser Ala Arg His Arg  
 370 375

&lt;210&gt; 189

&lt;211&gt; 160

&lt;212&gt; PRT

&lt;213&gt; Homo sapien

<400> 189  
 Met Leu Glu Ala His Arg Arg Gln Arg His Pro Phe Leu Leu Leu Gly  
 1 5 10 15  
 Thr Thr Ala Asn Arg Thr Gln Ser Leu Asn Tyr Gly Cys Ile Val Glu  
 20 25 30  
 Asn Pro Gln Thr His Glu Val Leu His Tyr Val Glu Lys Pro Ser Thr  
 35 40 45  
 Phe Ile Ser Asp Ile Ile Asn Cys Gly Ile Tyr Leu Phe Ser Pro Glu  
 50 55 60  
 Ala Leu Lys Pro Leu Arg Asp Val Phe Gln Arg Asn Gln Gln Asp Gly  
 65 70 75 80  
 Gln Leu Glu Asp Ser Pro Gly Leu Trp Pro Gly Ala Gly Thr Ile Arg  
 85 90 95  
 Leu Glu Gln Asp Val Phe Ser Ala Leu Ala Gly Gln Gly Gln Ile Tyr  
 100 105 110  
 Val His Leu Thr Asp Gly Ile Trp Ser Gln Ile Lys Ser Ala Gly Ser  
 115 120 125  
 Ala Leu Tyr Ala Ser Arg Leu Tyr Leu Ser Arg Tyr Gln Asp Thr His  
 130 135 140  
 Pro Glu Arg Leu Ala Lys His Thr Pro Gly Gly Pro Trp Ile Arg Gly  
 145 150 155 160

<210> 190  
 <211> 146  
 <212> PRT  
 <213> Homo sapien

<400> 190  
 Met Asp Pro Arg Ala Ser Leu Leu Leu Leu Gly Asn Val Tyr Ile His  
 1 5 10 15  
 Pro Thr Ala Lys Val Ala Pro Ser Ala Val Leu Gly Pro Asn Val Ser  
 20 25 30  
 Ile Gly Lys Gly Val Thr Val Gly Glu Gly Val Arg Leu Arg Glu Ser  
 35 40 45  
 Ile Val Leu His Gly Ala Thr Leu Gln Glu His Thr Cys Val Leu His  
 50 55 60  
 Ser Ile Val Gly Trp Gly Ser Thr Val Gly Arg Trp Ala Arg Val Glu  
 65 70 75 80  
 Gly Thr Pro Ser Asp Pro Asn Pro Asn Asp Pro Arg Ala Arg Met Asp  
 85 90 95  
 Ser Glu Ser Leu Phe Lys Asp Gly Lys Leu Leu Pro Ala Ile Thr Ile  
 100 105 110  
 Leu Gly Cys Arg Val Arg Ile Pro Ala Glu Val Leu Ile Leu Asn Ser  
 115 120 125  
 Ile Val Leu Pro His Lys Glu Leu Ser Arg Ser Phe Thr Asn Gln Ile  
 130 135 140  
 Ile Leu  
 145

<210> 191  
 <211> 704  
 <212> PRT  
 <213> Homo sapien



<400> 191

Glu	Gly	Gly	Cys	Ala	Ala	Gly	Arg	Gly	Arg	Glu	Leu	Glu	Pro	Glu	Leu	1	5	10	15
Glu	Pro	Gly	Pro	Gly	Pro	Gly	Ser	Ala	Leu	Glu	Pro	Gly	Glu	Glu	Phe	20	25	30	
Glu	Ile	Val	Asp	Arg	Ser	Gln	Leu	Pro	Gly	Pro	Gly	Asp	Leu	Arg	Ser	35	40	45	
Ala	Thr	Arg	Pro	Arg	Ala	Ala	Glu	Gly	Trp	Ser	Ala	Pro	Ile	Leu	Thr	50	55	60	
Leu	Ala	Arg	Arg	Ala	Thr	Gly	Asn	Leu	Ser	Ala	Ser	Cys	Gly	Ser	Ala	65	70	75	80
Leu	Arg	Ala	Ala	Ala	Gly	Leu	Gly	Gly	Gly	Asp	Ser	Gly	Asp	Gly	Thr	85	90	95	
Ala	Arg	Ala	Ala	Ser	Lys	Cys	Gln	Met	Met	Glu	Glu	Arg	Ala	Asn	Leu	100	105	110	
Met	His	Met	Met	Lys	Leu	Ser	Ile	Lys	Val	Leu	Leu	Gln	Ser	Ala	Leu	115	120	125	
Ser	Leu	Gly	Arg	Ser	Leu	Asp	Ala	Asp	His	Ala	Pro	Leu	Gln	Gln	Phe	130	135	140	
Phe	Val	Val	Met	Glu	His	Cys	Leu	Lys	His	Gly	Leu	Lys	Val	Lys	Lys	145	150	155	160
Ser	Phe	Ile	Gly	Gln	Asn	Lys	Ser	Phe	Phe	Gly	Pro	Leu	Glu	Leu	Val	165	170	175	
Glu	Lys	Leu	Cys	Pro	Glu	Ala	Ser	Asp	Ile	Ala	Thr	Ser	Val	Arg	Asn	180	185	190	
Leu	Pro	Glu	Leu	Lys	Thr	Ala	Val	Gly	Arg	Gly	Arg	Ala	Trp	Leu	Tyr	195	200	205	
Leu	Ala	Leu	Met	Gln	Lys	Lys	Leu	Ala	Asp	Tyr	Leu	Lys	Val	Leu	Ile	210	215	220	
Asp	Asn	Lys	His	Leu	Leu	Ser	Glu	Phe	Tyr	Glu	Pro	Glu	Ala	Leu	Met	225	230	235	240
Met	Glu	Glu	Glu	Gly	Met	Val	Ile	Val	Gly	Leu	Leu	Val	Gly	Leu	Asn	245	250	255	
Val	Leu	Asp	Ala	Asn	Leu	Cys	Leu	Lys	Gly	Glu	Asp	Leu	Asp	Ser	Gln	260	265	270	
Val	Gly	Val	Ile	Asp	Phe	Ser	Leu	Tyr	Leu	Lys	Asp	Val	Gln	Asp	Leu	275	280	285	
Asp	Gly	Gly	Lys	Glu	His	Glu	Arg	Ile	Thr	Asp	Val	Leu	Asp	Gln	Lys	290	295	300	
Asn	Tyr	Val	Glu	Glu	Leu	Asn	Arg	His	Leu	Ser	Cys	Thr	Val	Gly	Asp	305	310	315	320
Leu	Gln	Thr	Lys	Ile	Asp	Gly	Leu	Glu	Lys	Thr	Asn	Ser	Lys	Leu	Gln	325	330	335	
Glu	Glu	Leu	Ser	Ala	Ala	Thr	Asp	Arg	Ile	Cys	Ser	Leu	Gln	Glu	Glu	340	345	350	
Gln	Gln	Gln	Leu	Arg	Glu	Gln	Asn	Glu	Leu	Ile	Arg	Glu	Arg	Ser	Glu	355	360	365	
Lys	Ser	Val	Glu	Ile	Thr	Lys	Gln	Asp	Thr	Lys	Val	Glu	Leu	Glu	Thr	370	375	380	
Tyr	Lys	Gln	Thr	Arg	Gln	Gly	Leu	Asp	Glu	Met	Tyr	Ser	Asp	Val	Trp	385	390	395	400
Lys	Gln	Leu	Lys	Glu	Glu	Lys	Lys	Val	Arg	Leu	Glu	Leu	Glu	Lys	Glu	405	410	415	
Leu	Glu	Leu	Gln	Ile	Gly	Met	Lys	Thr	Glu	Met	Glu	Ile	Ala	Met	Lys	420	425	430	

Leu	Leu	Glu	Lys	Asp	Thr	His	Glu	Lys	Gln	Asp	Thr	Leu	Val	Ala	Leu
		435					440					445			
Arg	Gln	Gln	Leu	Glu	Glu	Val	Lys	Ala	Ile	Asn	Leu	Gln	Met	Phe	His
	450					455					460				
Lys	Ala	Gln	Asn	Ala	Glu	Ser	Ser	Leu	Gln	Gln	Lys	Asn	Glu	Ala	Ile
465					470					475					480
Thr	Ser	Phe	Glu	Gly	Lys	Thr	Asn	Gln	Val	Met	Ser	Ser	Met	Lys	Gln
				485					490					495	
Met	Glu	Glu	Arg	Leu	Gln	His	Ser	Glu	Arg	Ala	Arg	Gln	Gly	Ala	Glu
			500					505					510		
Glu	Arg	Ser	His	Lys	Leu	Gln	Gln	Glu	Leu	Gly	Gly	Arg	Ile	Gly	Ala
	515						520					525			
Leu	Gln	Leu	Gln	Leu	Ser	Gln	Leu	His	Glu	Gln	Cys	Ser	Ser	Leu	Glu
	530					535					540				
Lys	Glu	Leu	Lys	Ser	Glu	Lys	Glu	Gln	Arg	Gln	Ala	Leu	Gln	Arg	Glu
545					550				555						560
Leu	Gln	His	Glu	Lys	Asp	Thr	Ser	Ser	Leu	Leu	Arg	Met	Glu	Leu	Gln
				565					570					575	
Gln	Val	Glu	Gly	Leu	Lys	Lys	Glu	Leu	Arg	Glu	Leu	Gln	Asp	Glu	Lys
			580				585						590		
Ala	Glu	Leu	Gln	Lys	Ile	Cys	Glu	Glu	Gln	Glu	Gln	Ala	Leu	Gln	Glu
	595						600					605			
Met	Gly	Leu	His	Leu	Ser	Gln	Ser	Lys	Leu	Lys	Met	Glu	Asp	Ile	Lys
	610					615					620				
Glu	Val	Asn	Gln	Ala	Leu	Lys	Gly	His	Ala	Trp	Leu	Lys	Asp	Asp	Glu
625					630				635						640
Ala	Thr	His	Cys	Arg	Gln	Cys	Glu	Lys	Glu	Phe	Ser	Ile	Ser	Arg	Arg
				645					650					655	
Lys	His	His	Cys	Arg	Asn	Cys	Gly	His	Ile	Phe	Cys	Asn	Thr	Cys	Ser
			660				665						670		
Ser	Asn	Glu	Leu	Ala	Leu	Pro	Ser	Tyr	Pro	Lys	Pro	Val	Arg	Val	Cys
	675						680					685			
Asp	Ser	Cys	His	Thr	Leu	Leu	Leu	Gln	Arg	Cys	Ser	Ser	Thr	Ala	Ser
	690					695					700				

&lt;210&gt; 192

&lt;211&gt; 331

&lt;212&gt; PRT

&lt;213&gt; Homo sapien

&lt;400&gt; 192

Arg	Ala	Gly	Ala	Ser	Ala	Met	Ala	Leu	Arg	Lys	Glu	Leu	Leu	Lys	Ser
1				5					10					15	
Ile	Trp	Tyr	Ala	Phe	Thr	Ala	Leu	Asp	Val	Glu	Lys	Ser	Gly	Lys	Val
			20					25					30		
Ser	Lys	Ser	Gln	Leu	Lys	Val	Leu	Ser	His	Asn	Leu	Tyr	Thr	Val	Leu
		35					40					45			
His	Ile	Pro	His	Asp	Pro	Val	Ala	Leu	Glu	Glu	His	Phe	Arg	Asp	Asp
	50					55					60				
Asp	Asp	Gly	Pro	Val	Ser	Ser	Gln	Gly	Tyr	Met	Pro	Tyr	Leu	Asn	Lys
65					70				75					80	
Tyr	Ile	Leu	Asp	Lys	Val	Glu	Glu	Gly	Ala	Phe	Val	Lys	Glu	His	Phe
				85					90					95	
Asp	Glu	Leu	Cys	Trp	Thr	Leu	Thr	Ala	Lys	Lys	Asn	Tyr	Arg	Ala	Asp
			100					105					110		

Ser	Asn	Gly	Asn	Ser	Met	Leu	Ser	Asn	Gln	Asp	Ala	Phe	Arg	Leu	Trp
		115						120				125			
Cys	Leu	Phe	Asn	Phe	Leu	Ser	Glu	Asp	Lys	Tyr	Pro	Leu	Ile	Met	Val
	130					135					140				
Pro	Asp	Glu	Val	Glu	Tyr	Leu	Leu	Lys	Lys	Val	Leu	Ser	Ser	Met	Ser
145					150					155					160
Leu	Glu	Val	Ser	Leu	Gly	Glu	Leu	Glu	Glu	Leu	Leu	Ala	Gln	Glu	Ala
				165					170					175	
Gln	Val	Ala	Gln	Thr	Thr	Gly	Gly	Leu	Ser	Val	Trp	Gln	Phe	Leu	Glu
			180					185					190		
Leu	Phe	Asn	Ser	Gly	Arg	Cys	Leu	Arg	Gly	Val	Gly	Arg	Asp	Thr	Leu
		195				200						205			
Ser	Met	Ala	Ile	His	Glu	Val	Tyr	Gln	Glu	Leu	Ile	Gln	Asp	Val	Leu
	210					215					220				
Lys	Gln	Gly	Tyr	Leu	Trp	Lys	Arg	Gly	His	Leu	Arg	Arg	Asn	Trp	Ala
225					230					235					240
Glu	Arg	Trp	Phe	Gln	Leu	Gln	Pro	Ser	Cys	Leu	Cys	Tyr	Phe	Gly	Ser
				245					250					255	
Glu	Glu	Cys	Lys	Glu	Lys	Arg	Gly	Ile	Ile	Pro	Leu	Asp	Ala	His	Cys
			260					265					270		
Cys	Val	Glu	Val	Leu	Pro	Asp	Arg	Asp	Gly	Lys	Arg	Cys	Met	Phe	Cys
		275					280					285			
Val	Lys	Thr	Ala	Thr	Arg	Thr	Tyr	Glu	Met	Ser	Ala	Ser	Asp	Thr	Arg
	290					295					300				
Gln	Arg	Gln	Glu	Trp	Thr	Ala	Ala	Ile	Gln	Met	Ala	Ile	Arg	Leu	Gln
305					310					315					320
Ala	Glu	Gly	Lys	Thr	Ser	Leu	His	Lys	Asp	Leu					
				325					330						

&lt;210&gt; 193

&lt;211&gt; 475

&lt;212&gt; PRT

&lt;213&gt; Homo sapien

&lt;400&gt; 193

Lys	Asn	Ser	Pro	Leu	Leu	Ser	Val	Ser	Ser	Gln	Thr	Ile	Thr	Lys	Glu
1				5					10					15	
Asn	Asn	Arg	Asn	Val	His	Leu	Glu	His	Ser	Glu	Gln	Asn	Pro	Gly	Ser
			20					25					30		
Ser	Ala	Gly	Asp	Thr	Ser	Ala	Ala	His	Gln	Val	Val	Leu	Gly	Glu	Asn
	35					40						45			
Leu	Ile	Ala	Thr	Ala	Leu	Cys	Leu	Ser	Gly	Ser	Gly	Ser	Gln	Ser	Asp
	50					55					60				
Leu	Lys	Asp	Val	Ala	Ser	Thr	Ala	Gly	Glu	Glu	Gly	Asp	Thr	Ser	Leu
65					70					75					80
Arg	Glu	Ser	Leu	His	Pro	Val	Thr	Arg	Ser	Leu	Lys	Ala	Gly	Cys	His
				85					90					95	
Thr	Lys	Gln	Leu	Ala	Ser	Arg	Asn	Cys	Ser	Glu	Glu	Lys	Ser	Pro	Gln
			100					105					110		
Thr	Ser	Ile	Leu	Lys	Glu	Gly	Asn	Arg	Asp	Thr	Ser	Leu	Asp	Phe	Arg
	115					120						125			
Pro	Val	Val	Ser	Pro	Ala	Asn	Gly	Val	Glu	Gly	Val	Arg	Val	Asp	Gln
	130					135						140			
Asp	Asp	Asp	Gln	Asp	Ser	Ser	Ser	Leu	Lys	Leu	Ser	Gln	Asn	Ile	Ala
145					150					155					160

Val	Gln	Thr	Asp	Phe	Lys	Thr	Ala	Asp	Ser	Glu	Val	Asn	Thr	Asp	Gln
				165					170					175	
Asp	Ile	Glu	Lys	Asn	Leu	Asp	Lys	Met	Met	Thr	Glu	Arg	Thr	Leu	Leu
			180					185						190	
Lys	Glu	Arg	Tyr	Gln	Glu	Val	Leu	Asp	Lys	Gln	Arg	Gln	Val	Glu	Asn
		195					200					205			
Gln	Leu	Gln	Val	Gln	Leu	Lys	Gln	Leu	Gln	Gln	Arg	Arg	Glu	Glu	Glu
	210					215					220				
Met	Lys	Asn	His	Gln	Glu	Ile	Leu	Lys	Ala	Ile	Gln	Asp	Val	Thr	Ile
225					230					235					240
Lys	Arg	Glu	Glu	Thr	Lys	Lys	Lys	Ile	Glu	Lys	Glu	Lys	Lys	Glu	Phe
				245					250					255	
Leu	Gln	Lys	Glu	Gln	Asp	Leu	Lys	Ala	Glu	Ile	Glu	Lys	Leu	Cys	Glu
			260					265					270		
Lys	Gly	Arg	Arg	Glu	Val	Trp	Glu	Met	Glu	Leu	Asp	Arg	Leu	Lys	Asn
	275						280					285			
Gln	Asp	Gly	Glu	Ile	Asn	Arg	Asn	Ile	Met	Glu	Glu	Thr	Glu	Arg	Ala
	290					295					300				
Trp	Lys	Ala	Glu	Ile	Leu	Ser	Leu	Glu	Ser	Arg	Lys	Glu	Leu	Leu	Val
305					310					315					320
Leu	Lys	Leu	Glu	Glu	Ala	Glu	Lys	Glu	Ala	Glu	Leu	His	Leu	Thr	Tyr
				325					330					335	
Leu	Lys	Ser	Thr	Pro	Pro	Thr	Leu	Glu	Thr	Val	Arg	Ser	Lys	Gln	Glu
			340					345					350		
Trp	Glu	Thr	Arg	Leu	Asn	Gly	Val	Arg	Ile	Met	Lys	Lys	Asn	Val	Arg
	355						360					365			
Asp	Gln	Phe	Asn	Ser	His	Ile	Gln	Leu	Val	Arg	Asn	Gly	Ala	Lys	Leu
	370					375					380				
Ser	Ser	Leu	Pro	Gln	Ile	Pro	Thr	Pro	Thr	Leu	Pro	Pro	Pro	Pro	Ser
385					390					395					400
Glu	Thr	Asp	Phe	Met	Leu	Gln	Val	Phe	Gln	Pro	Ser	Pro	Ser	Leu	Ala
				405					410					415	
Pro	Arg	Met	Pro	Phe	Ser	Ile	Gly	Gln	Val	Thr	Met	Pro	Met	Val	Met
			420					425					430		
Pro	Ser	Ala	Asp	Pro	Arg	Ser	Leu	Ser	Phe	Pro	Ile	Leu	Asn	Pro	Ala
	435						440					445			
Leu	Ser	Gln	Pro	Ser	Gln	Pro	Ser	Ser	Pro	Leu	Pro	Gly	Ser	His	Gly
	450					455					460				
Arg	Asn	Ser	Pro	Gly	Leu	Gly	Ser	Leu	Val	Ser					
465					470					475					

&lt;210&gt; 194

&lt;211&gt; 241

&lt;212&gt; PRT

&lt;213&gt; Homo sapien

&lt;400&gt; 194

Met	Ser	Gly	Glu	Ser	Ala	Arg	Ser	Leu	Gly	Lys	Gly	Ser	Ala	Pro	Pro
1				5					10					15	
Gly	Pro	Val	Pro	Glu	Gly	Ser	Ile	Arg	Ile	Tyr	Ser	Met	Arg	Phe	Cys
			20					25					30		
Pro	Phe	Ala	Glu	Arg	Thr	Arg	Leu	Val	Leu	Lys	Ala	Lys	Gly	Ile	Arg
	35						40					45			
His	Glu	Val	Ile	Asn	Ile	Asn	Leu	Lys	Asn	Lys	Pro	Glu	Trp	Phe	Phe
50						55					60				

92

Lys Lys Asn Pro Phe Gly Leu Val Pro Val Leu Glu Asn Ser Gln Gly  
 65 70 75 80  
 Gln Leu Ile Tyr Glu Ser Ala Ile Thr Cys Glu Tyr Leu Asp Glu Ala  
 85 90 95  
 Tyr Pro Gly Lys Lys Leu Leu Pro Asp Asp Pro Tyr Glu Lys Ala Cys  
 100 105 110  
 Gln Lys Met Ile Leu Glu Leu Phe Ser Lys Val Pro Ser Leu Val Gly  
 115 120 125  
 Ser Phe Ile Arg Ser Gln Asn Lys Glu Asp Tyr Ala Gly Leu Lys Glu  
 130 135 140  
 Glu Phe Arg Lys Glu Phe Thr Lys Leu Glu Glu Val Leu Thr Asn Lys  
 145 150 155 160  
 Lys Thr Thr Phe Phe Gly Gly Asn Ser Ile Ser Met Ile Asp Tyr Leu  
 165 170 175  
 Ile Trp Pro Trp Phe Glu Arg Leu Glu Ala Met Lys Leu Asn Glu Cys  
 180 185 190  
 Val Asp His Thr Pro Lys Leu Lys Leu Trp Met Ala Ala Met Lys Glu  
 195 200 205  
 Asp Pro Thr Val Ser Ala Leu Leu Thr Ser Glu Lys Asp Trp Gln Gly  
 210 215 220  
 Phe Leu Glu Leu Tyr Leu Gln Asn Ser Pro Glu Ala Cys Asp Tyr Gly  
 225 230 235 240  
 Leu

<210> 195  
 <211> 138  
 <212> PRT  
 <213> Homo sapien

<400> 195  
 Gln Thr Lys Ile Leu Glu Glu Asp Leu Glu Gln Ile Lys Leu Ser Leu  
 1 5 10 15  
 Arg Glu Arg Gly Arg Glu Leu Thr Thr Gln Arg Gln Leu Met Gln Glu  
 20 25 30  
 Arg Ala Glu Glu Gly Lys Gly Pro Ser Lys Ala Gln Arg Gly Ser Leu  
 35 40 45  
 Glu His Met Lys Leu Ile Leu Arg Asp Lys Glu Lys Glu Val Glu Cys  
 50 55 60  
 Gln Gln Glu His Ile His Glu Leu Gln Glu Leu Lys Asp Gln Leu Glu  
 65 70 75 80  
 Gln Gln Leu Gln Gly Leu His Arg Lys Val Gly Glu Thr Ser Leu Leu  
 85 90 95  
 Leu Ser Gln Arg Glu Gln Glu Ile Val Val Leu Gln Gln Gln Leu Gln  
 100 105 110  
 Glu Ala Arg Glu Gln Gly Glu Leu Lys Glu Gln Ser Leu Gln Ser Gln  
 115 120 125  
 Leu Asp Glu Ala Gln Arg Ala Leu Ala Gln  
 130 135

<210> 196  
 <211> 102  
 <212> PRT  
 <213> Homo sapien

<400> 196  
 Met Ser Lys Arg Lys Ala Pro Gln Glu Thr Leu Asn Gly Gly Ile Thr  
 1 5 10 15  
 Asp Met Leu Thr Glu Leu Ala Asn Phe Glu Lys Asn Val Ser Gln Ala  
 20 25 30  
 Ile His Lys Tyr Asn Ala Tyr Arg Lys Ala Ala Ser Val Ile Ala Lys  
 35 40 45  
 Tyr Pro His Lys Ile Lys Ser Gly Ala Glu Ala Lys Lys Leu Pro Gly  
 50 55 60  
 Val Gly Thr Lys Ile Ala Glu Lys Ile Asp Glu Phe Leu Ala Thr Gly  
 65 70 75 80  
 Lys Leu Arg Lys Leu Glu Lys Ile Arg Gln Asp Asp Thr Ser Ser Ser  
 85 90 95  
 Ile Asn Phe Leu Thr Arg  
 100

<210> 197  
 <211> 138  
 <212> PRT  
 <213> Homo sapien

<400> 197  
 Glu Ala Asn Glu Val Thr Asp Ser Ala Tyr Met Gly Ser Glu Ser Thr  
 1 5 10 15  
 Tyr Ser Glu Cys Glu Thr Phe Thr Asp Glu Asp Thr Ser Thr Leu Val  
 20 25 30  
 His Pro Glu Leu Gln Pro Glu Gly Asp Ala Asp Ser Ala Gly Gly Ser  
 35 40 45  
 Ala Val Pro Ser Glu Cys Leu Asp Ala Met Glu Glu Pro Asp His Gly  
 50 55 60  
 Ala Leu Leu Leu Leu Pro Gly Arg Pro His Pro His Gly Gln Ser Val  
 65 70 75 80  
 Ile Thr Val Ile Gly Gly Glu Glu His Phe Glu Asp Tyr Gly Glu Gly  
 85 90 95  
 Ser Glu Ala Glu Leu Ser Pro Glu Thr Leu Cys Asn Gly Gln Leu Gly  
 100 105 110  
 Cys Ser Asp Pro Ala Phe Leu Thr Pro Ser Pro Thr Lys Arg Leu Ser  
 115 120 125  
 Ser Lys Lys Val Ala Arg Tyr Leu His Gln  
 130 135

<210> 198  
 <211> 100  
 <212> PRT  
 <213> Homo sapien

<400> 198  
 Met Gly Asp Val Lys Asn Phe Leu Tyr Ala Trp Cys Gly Lys Arg Lys  
 1 5 10 15  
 Met Thr Pro Ser Tyr Glu Ile Arg Ala Val Gly Asn Lys Asn Arg Gln  
 20 25 30  
 Lys Phe Met Cys Glu Val Gln Val Glu Gly Tyr Asn Tyr Thr Gly Met  
 35 40 45  
 Gly Asn Ser Thr Asn Lys Lys Asp Ala Gln Ser Asn Ala Ala Arg Asp  
 50 55 60



Phe Val Asn Tyr Leu Val Arg Ile Asn Glu Ile Lys Ser Glu Glu Val  
 65 70 75 80  
 Pro Ala Phe Gly Val Ala Ser Pro Pro Pro Leu Thr Asp Thr Pro Asp  
 85 90 95  
 Thr Thr Ala Asn  
 100

<210> 199  
 <211> 127  
 <212> PRT  
 <213> Homo sapien

<400> 199  
 Met Val Lys Glu Thr Thr Tyr Tyr Asp Val Leu Gly Val Lys Pro Asn  
 1 5 10 15  
 Ala Thr Gln Glu Glu Leu Lys Lys Ala Tyr Arg Lys Leu Ala Leu Lys  
 20 25 30  
 Tyr His Pro Asp Lys Asn Pro Asn Glu Gly Glu Lys Phe Lys Gln Ile  
 35 40 45  
 Ser Gln Ala Tyr Glu Val Leu Ser Asp Ala Lys Lys Arg Glu Leu Tyr  
 50 55 60  
 Asp Lys Gly Gly Glu Gln Ala Ile Lys Glu Gly Gly Ala Gly Gly Gly  
 65 70 75 80  
 Phe Gly Ser Pro Met Asp Ile Phe Asp Met Phe Phe Gly Gly Gly Gly  
 85 90 95  
 Arg Met Gln Arg Glu Arg Arg Gly Lys Asn Val Val His Gln Leu Ser  
 100 105 110  
 Val Thr Leu Glu Asp Leu Tyr Asn Gly Ala Thr Arg Lys Leu Ala  
 115 120 125

<210> 200  
 <211> 90  
 <212> PRT  
 <213> Homo sapien

<400> 200  
 Met Ala Cys Pro Leu Asp Gln Ala Ile Gly Leu Leu Val Ala Ile Phe  
 1 5 10 15  
 His Lys Tyr Ser Gly Arg Glu Gly Asp Lys His Thr Leu Ser Lys Lys  
 20 25 30  
 Glu Leu Lys Glu Leu Ile Gln Lys Glu Leu Thr Ile Gly Ser Lys Leu  
 35 40 45  
 Gln Asp Ala Glu Ile Ala Arg Leu Met Glu Asp Leu Asp Arg Asn Lys  
 50 55 60  
 Asp Gln Glu Val Asn Phe Gln Glu Tyr Val Thr Phe Leu Gly Ala Leu  
 65 70 75 80  
 Ala Leu Ile Tyr Asn Glu Ala Leu Lys Gly  
 85 90

<210> 201  
 <211> 120  
 <212> PRT  
 <213> Homo sapien

<400> 201

95

Met	Glu	Thr	Pro	Ser	Gln	Arg	Arg	Ala	Thr	Arg	Ser	Gly	Ala	Gln	Ala
1				5					10					15	
Ser	Ser	Thr	Pro	Leu	Ser	Pro	Thr	Arg	Ile	Thr	Arg	Leu	Gln	Glu	Lys
			20					25					30		
Glu	Asp	Leu	Gln	Glu	Leu	Asn	Asp	Arg	Leu	Ala	Val	Tyr	Ile	Asp	Arg
	35						40					45			
Val	Arg	Ser	Leu	Glu	Thr	Glu	Asn	Ala	Gly	Leu	Arg	Leu	Arg	Ile	Thr
	50					55					60				
Glu	Ser	Glu	Glu	Val	Val	Ser	Arg	Glu	Val	Ser	Gly	Ile	Lys	Ala	Ala
65					70					75					80
Tyr	Glu	Ala	Glu	Leu	Gly	Asp	Ala	Arg	Lys	Thr	Leu	Asp	Ser	Val	Ala
				85					90					95	
Lys	Glu	Arg	Ala	Arg	Leu	Gln	Leu	Glu	Leu	Ser	Lys	Val	Arg	Glu	Glu
			100					105						110	
Phe	Lys	Glu	Leu	Lys	Ala	Arg	Asn								
			115				120								

&lt;210&gt; 202

&lt;211&gt; 177

&lt;212&gt; PRT

&lt;213&gt; Homo sapien

&lt;400&gt; 202

Met	Ala	Ala	Gly	Val	Glu	Ala	Ala	Ala	Glu	Val	Ala	Ala	Thr	Glu	Ile
1				5					10					15	
Lys	Met	Glu	Glu	Glu	Ser	Gly	Ala	Pro	Gly	Val	Pro	Ser	Gly	Asn	Gly
			20					25					30		
Ala	Pro	Gly	Pro	Lys	Gly	Glu	Gly	Glu	Arg	Pro	Ala	Gln	Asn	Glu	Lys
	35						40					45			
Arg	Lys	Glu	Lys	Asn	Ile	Lys	Arg	Gly	Gly	Asn	Arg	Phe	Glu	Pro	Tyr
	50					55					60				
Ala	Asn	Pro	Thr	Lys	Arg	Tyr	Arg	Ala	Phe	Ile	Thr	Asn	Ile	Pro	Phe
65					70					75					80
Asp	Val	Lys	Trp	Gln	Ser	Leu	Lys	Asp	Leu	Val	Lys	Glu	Lys	Val	Gly
			85					90						95	
Glu	Val	Thr	Tyr	Val	Glu	Leu	Leu	Met	Asp	Ala	Glu	Gly	Lys	Ser	Arg
			100					105					110		
Gly	Cys	Ala	Val	Val	Glu	Phe	Lys	Met	Glu	Glu	Ser	Met	Lys	Lys	Ala
		115					120					125			
Ala	Glu	Val	Leu	Asn	Lys	His	Ser	Leu	Ser	Gly	Arg	Pro	Leu	Lys	Val
	130					135					140				
Lys	Glu	Asp	Pro	Asp	Gly	Glu	His	Ala	Arg	Arg	Ala	Met	Gln	Lys	Ala
145					150					155					160
Gly	Arg	Leu	Gly	Ser	Thr	Val	Phe	Val	Ala	Asn	Leu	Asp	Tyr	Lys	Val
				165					170					175	

Gly

&lt;210&gt; 203

&lt;211&gt; 164

&lt;212&gt; PRT

&lt;213&gt; Homo sapien

&lt;400&gt; 203

Met	Arg	Leu	Ala	Val	Gly	Ala	Leu	Leu	Val	Cys	Ala	Val	Leu	Gly	Leu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

96

1				5					10					15			
Cys	Leu	Ala	Val	Pro	Asp	Lys	Thr	Val	Arg	Trp	Cys	Ala	Val	Ser	Glu		
			20						25					30			
His	Glu	Ala	Thr	Lys	Cys	Gln	Ser	Phe	Arg	Asp	His	Met	Lys	Ser	Val		
		35							40					45			
Ile	Pro	Ser	Asp	Gly	Pro	Ser	Val	Ala	Cys	Val	Lys	Lys	Ala	Ser	Tyr		
	50					55					60						
Leu	Asp	Cys	Ile	Arg	Ala	Ile	Ala	Ala	Asn	Glu	Ala	Asp	Ala	Val	Thr		
65					70					75					80		
Leu	Asp	Ala	Gly	Leu	Val	Tyr	Asp	Ala	Tyr	Leu	Ala	Pro	Asn	Asn	Leu		
				85					90					95			
Lys	Pro	Val	Val	Ala	Glu	Phe	Tyr	Gly	Ser	Lys	Glu	Asp	Pro	Gln	Thr		
			100						105					110			
Phe	Tyr	Tyr	Ala	Val	Ala	Val	Val	Lys	Lys	Asp	Ser	Gly	Phe	Gln	Met		
		115					120					125					
Asn	Gln	Leu	Arg	Gly	Lys	Lys	Ser	Cys	His	Thr	Gly	Leu	Gly	Arg	Ser		
	130					135					140						
Ala	Gly	Trp	Asn	Ile	Pro	Ile	Gly	Leu	Leu	Tyr	Cys	Asp	Leu	Pro	Glu		
145					150				155						160		
Pro	Arg	Lys	Pro														

&lt;210&gt; 204

&lt;211&gt; 241

&lt;212&gt; PRT

&lt;213&gt; Homo sapien

&lt;400&gt; 204

Met	Ser	Gly	Glu	Ser	Ala	Arg	Ser	Leu	Gly	Lys	Gly	Ser	Ala	Pro	Pro		
1				5					10					15			
Gly	Pro	Val	Pro	Glu	Gly	Ser	Ile	Arg	Ile	Tyr	Ser	Met	Arg	Phe	Cys		
			20					25					30				
Pro	Phe	Ala	Glu	Arg	Thr	Arg	Leu	Val	Leu	Lys	Ala	Lys	Gly	Ile	Arg		
		35					40					45					
His	Glu	Val	Ile	Asn	Ile	Asn	Leu	Lys	Asn	Lys	Pro	Glu	Trp	Phe	Phe		
	50					55					60						
Lys	Lys	Asn	Pro	Phe	Gly	Leu	Val	Pro	Val	Leu	Glu	Asn	Ser	Gln	Gly		
65					70				75					80			
Gln	Leu	Ile	Tyr	Glu	Ser	Ala	Ile	Thr	Cys	Glu	Tyr	Leu	Asp	Glu	Ala		
				85					90					95			
Tyr	Pro	Gly	Lys	Lys	Leu	Leu	Pro	Asp	Asp	Pro	Tyr	Glu	Lys	Ala	Cys		
			100					105					110				
Gln	Lys	Met	Ile	Leu	Glu	Leu	Phe	Ser	Lys	Val	Pro	Ser	Leu	Val	Gly		
		115					120					125					
Ser	Phe	Ile	Arg	Ser	Gln	Asn	Lys	Glu	Asp	Tyr	Asp	Gly	Leu	Lys	Glu		
	130					135					140						
Glu	Phe	Arg	Lys	Glu	Phe	Thr	Lys	Leu	Glu	Glu	Val	Leu	Thr	Asn	Lys		
145					150				155						160		
Lys	Thr	Thr	Phe	Phe	Gly	Gly	Asn	Ser	Ile	Ser	Met	Ile	Asp	Tyr	Leu		
			165					170					175				
Ile	Trp	Pro	Trp	Phe	Glu	Arg	Leu	Glu	Ala	Met	Lys	Leu	Asn	Glu	Cys		
		180						185					190				
Val	Asp	His	Thr	Pro	Lys	Leu	Lys	Leu	Trp	Met	Ala	Ala	Met	Lys	Glu		
	195					200					205						
Asp	Pro	Thr	Val	Ser	Ala	Leu	Leu	Thr	Ser	Glu	Lys	Asp	Trp	Gln	Gly		

210		215		220											
Phe	Leu	Glu	Leu	Tyr	Leu	Gln	Asn	Ser	Pro	Glu	Ala	Cys	Asp	Tyr	Gly
225			230							235					240
Leu															

<210> 205  
 <211> 160  
 <212> PRT  
 <213> Homo sapien

<400> 205															
Met	Gln	Ile	Phe	Val	Lys	Thr	Leu	Thr	Gly	Lys	Thr	Ile	Thr	Leu	Glu
1				5					10					15	
Val	Glu	Pro	Ser	Asp	Thr	Ile	Glu	Asn	Val	Lys	Ala	Lys	Ile	Gln	Asp
			20					25					30		
Lys	Glu	Gly	Ile	Pro	Pro	Asp	Gln	Gln	Arg	Leu	Ile	Phe	Ala	Gly	Lys
		35					40					45			
Gln	Leu	Glu	Asp	Gly	Arg	Thr	Leu	Ser	Asp	Tyr	Asn	Ile	Gln	Lys	Glu
	50					55					60				
Ser	Thr	Leu	His	Leu	Val	Leu	Arg	Leu	Arg	Gly	Gly	Met	Gln	Ile	Phe
65				70					75						80
Val	Lys	Thr	Leu	Thr	Gly	Lys	Thr	Ile	Thr	Leu	Glu	Val	Glu	Pro	Ser
			85						90					95	
Asp	Thr	Ile	Glu	Asn	Val	Lys	Ala	Lys	Ile	Gln	Asp	Lys	Glu	Gly	Ile
			100					105					110		
Pro	Pro	Asp	Gln	Gln	Arg	Leu	Ile	Phe	Ala	Gly	Lys	Gln	Leu	Glu	Asp
		115					120					125			
Gly	Arg	Thr	Leu	Ser	Asp	Tyr	Asn	Ile	Gln	Lys	Glu	Ser	Thr	Leu	His
	130					135					140				
Leu	Val	Leu	Arg	Leu	Arg	Gly	Gly	Met	Gln	Ile	Phe	Val	Lys	Thr	Leu
145					150					155					160

<210> 206  
 <211> 197  
 <212> PRT  
 <213> Homo sapien

<400> 206															
Thr	Ser	Pro	Ser	Glu	Ala	Cys	Ala	Pro	Leu	Leu	Ile	Ser	Leu	Ser	Thr
1				5					10					15	
Leu	Ile	Tyr	Asn	Gly	Ala	Leu	Pro	Cys	Gln	Cys	Asn	Pro	Gln	Gly	Ser
			20					25					30		
Leu	Ser	Ser	Glu	Cys	Asn	Pro	His	Gly	Gly	Gln	Cys	Leu	Cys	Lys	Pro
		35					40					45			
Gly	Val	Val	Gly	Arg	Arg	Cys	Asp	Leu	Cys	Ala	Pro	Gly	Tyr	Tyr	Gly
	50					55					60				
Phe	Gly	Pro	Thr	Gly	Cys	Gln	Gly	Ala	Cys	Leu	Gly	Cys	Arg	Asp	His
65				70					75						80
Thr	Gly	Gly	Glu	His	Cys	Glu	Arg	Cys	Ile	Ala	Gly	Phe	His	Gly	Asp
			85						90					95	
Pro	Arg	Leu	Pro	Tyr	Gly	Gly	Gln	Cys	Arg	Pro	Cys	Pro	Cys	Pro	Glu
		100						105				110			
Gly	Pro	Gly	Ser	Gln	Arg	His	Phe	Ala	Thr	Ser	Cys	His	Gln	Asp	Glu
		115					120					125			

98

Tyr Ser Gln Gln Ile Val Cys His Cys Arg Ala Gly Tyr Thr Gly Leu  
 130 135 140  
 Arg Cys Glu Ala Cys Ala Pro Gly His Phe Gly Asp Pro Ser Arg Pro  
 145 150 155 160  
 Gly Gly Arg Cys Gln Leu Cys Glu Cys Ser Gly Asn Ile Asp Pro Met  
 165 170 175  
 Asp Pro Asp Ala Cys Asp Pro His Thr Gly Gln Cys Leu Arg Cys Leu  
 180 185 190  
 His His Thr Glu Gly  
 195

<210> 207  
 <211> 175  
 <212> PRT  
 <213> Homo sapien

<400> 207  
 Ile Ile Arg Gln Gln Gly Leu Ala Ser Tyr Asp Tyr Val Arg Arg Arg  
 1 5 10 15  
 Leu Thr Ala Glu Asp Leu Phe Glu Ala Arg Ile Ile Ser Leu Glu Thr  
 20 25 30  
 Tyr Asn Leu Leu Arg Glu Gly Thr Arg Ser Leu Arg Glu Ala Leu Glu  
 35 40 45  
 Ala Glu Ser Ala Trp Cys Tyr Leu Tyr Gly Thr Gly Ser Val Ala Gly  
 50 55 60  
 Val Tyr Leu Pro Gly Ser Arg Gln Thr Leu Ser Ile Tyr Gln Ala Leu  
 65 70 75 80  
 Lys Lys Gly Leu Leu Ser Ala Glu Val Ala Arg Leu Leu Leu Glu Ala  
 85 90 95  
 Gln Ala Ala Thr Gly Phe Leu Leu Asp Pro Val Lys Gly Glu Arg Leu  
 100 105 110  
 Thr Val Asp Glu Ala Val Arg Lys Gly Leu Val Gly Pro Glu Leu His  
 115 120 125  
 Asp Arg Leu Leu Ser Ala Glu Arg Ala Val Thr Gly Tyr Arg Asp Pro  
 130 135 140  
 Tyr Thr Glu Gln Thr Ile Ser Leu Phe Gln Ala Met Lys Lys Glu Leu  
 145 150 155 160  
 Ile Pro Thr Glu Glu Ala Leu Arg Leu Trp Met Pro Ser Trp Pro  
 165 170 175

<210> 208  
 <211> 177  
 <212> PRT  
 <213> Homo sapien

<400> 208  
 Met Ala Ala Gly Val Glu Ala Ala Ala Glu Val Ala Ala Thr Glu Ile  
 1 5 10 15  
 Lys Met Glu Glu Glu Ser Gly Ala Pro Gly Val Pro Ser Gly Asn Gly  
 20 25 30  
 Ala Pro Gly Pro Lys Gly Glu Gly Glu Arg Pro Ala Gln Asn Glu Lys  
 35 40 45  
 Arg Lys Glu Lys Asn Ile Lys Arg Gly Gly Asn Arg Phe Glu Pro Tyr  
 50 55 60  
 Ala Asn Pro Thr Lys Arg Tyr Arg Ala Phe Ile Thr Asn Ile Pro Phe

99

65					70					75					80
Asp	Val	Lys	Trp	Gln	Ser	Leu	Lys	Asp	Leu	Val	Lys	Glu	Lys	Val	Gly
				85					90					95	
Glu	Val	Thr	Tyr	Val	Glu	Leu	Leu	Met	Asp	Ala	Glu	Gly	Lys	Ser	Arg
			100					105					110		
Gly	Cys	Ala	Val	Val	Glu	Phe	Lys	Met	Glu	Glu	Ser	Met	Lys	Lys	Ala
		115					120					125			
Ala	Glu	Val	Leu	Asn	Lys	His	Ser	Leu	Ser	Gly	Arg	Pro	Leu	Lys	Val
		130				135					140				
Lys	Glu	Asp	Pro	Asp	Gly	Glu	His	Ala	Arg	Arg	Ala	Met	Gln	Lys	Val
145					150				155					160	
Met	Ala	Thr	Thr	Gly	Gly	Met	Gly	Met	Gly	Pro	Gly	Gly	Pro	Gly	Met
				165					170					175	

Ile

<210> 209  
 <211> 196  
 <212> PRT  
 <213> Homo sapien

<400> 209

Asp	Leu	Gln	Asp	Met	Phe	Ile	Val	His	Thr	Ile	Glu	Glu	Ile	Glu	Gly
1				5					10					15	
Leu	Ile	Ser	Ala	His	Asp	Gln	Phe	Lys	Ser	Thr	Leu	Pro	Asp	Ala	Asp
			20					25					30		
Arg	Glu	Arg	Glu	Ala	Ile	Leu	Ala	Ile	His	Lys	Glu	Ala	Gln	Arg	Ile
		35					40					45			
Ala	Glu	Ser	Asn	His	Ile	Lys	Leu	Ser	Gly	Ser	Asn	Pro	Tyr	Thr	Thr
	50					55					60				
Val	Thr	Pro	Gln	Ile	Ile	Asn	Ser	Lys	Trp	Glu	Lys	Val	Gln	Gln	Leu
65					70				75					80	
Val	Pro	Lys	Arg	Asp	His	Ala	Leu	Leu	Glu	Glu	Gln	Ser	Lys	Gln	Gln
			85						90				95		
Ser	Asn	Glu	His	Leu	Arg	Arg	Gln	Phe	Ala	Ser	Gln	Ala	Asn	Val	Val
		100						105					110		
Gly	Pro	Trp	Ile	Gln	Thr	Lys	Met	Glu	Glu	Ile	Gly	Arg	Ile	Ser	Ile
		115				120						125			
Glu	Met	Asn	Gly	Thr	Leu	Glu	Asp	Gln	Leu	Ser	His	Leu	Lys	Gln	Tyr
	130					135					140				
Glu	Arg	Ser	Ile	Val	Asp	Tyr	Lys	Pro	Asn	Leu	Asp	Leu	Leu	Glu	Gln
145					150				155					160	
Gln	His	Gln	Leu	Ile	Gln	Glu	Ala	Leu	Ile	Phe	Asp	Asn	Lys	His	Thr
			165						170					175	
Asn	Tyr	Thr	Met	Glu	His	Ile	Arg	Val	Gly	Trp	Glu	Gln	Leu	Leu	Thr
		180						185					190		

Thr Ile Ala Arg  
 195

<210> 210  
 <211> 156  
 <212> PRT  
 <213> Homo sapien

<400> 210



100

Lys	Leu	Thr	Ile	Glu	Ser	Thr	Pro	Phe	Asn	Val	Ala	Glu	Gly	Lys	Glu
1				5					10					15	
Val	Leu	Leu	Leu	Ala	His	Asn	Leu	Pro	Gln	Asn	Arg	Ile	Gly	Tyr	Ser
			20					25					30		
Trp	Tyr	Lys	Gly	Glu	Arg	Val	Asp	Gly	Asn	Ser	Leu	Ile	Val	Gly	Tyr
	35						40					45			
Val	Ile	Gly	Thr	Gln	Gln	Ala	Thr	Pro	Gly	Pro	Ala	Tyr	Ser	Gly	Arg
	50					55					60				
Glu	Thr	Ile	Tyr	Pro	Asn	Ala	Ser	Leu	Leu	Ile	Gln	Asn	Val	Thr	Gln
65					70					75					80
Asn	Asp	Thr	Gly	Phe	Tyr	Thr	Leu	Gln	Val	Ile	Lys	Ser	Asp	Leu	Val
			85					90					95		
Asn	Glu	Glu	Ala	Thr	Gly	Gln	Phe	His	Val	Tyr	Pro	Glu	Leu	Pro	Lys
			100					105					110		
Pro	Ser	Ile	Ser	Ser	Asn	Asn	Ser	Asn	Pro	Val	Glu	Asp	Lys	Asp	Ala
		115					120					125			
Val	Ala	Phe	Thr	Cys	Glu	Pro	Glu	Val	Gln	Asn	Thr	Thr	Tyr	Leu	Trp
	130					135					140				
Trp	Val	Asn	Gly	Gln	Ser	Leu	Pro	Val	Ser	Pro	Lys				
145					150					155					

<210> 211  
 <211> 92  
 <212> PRT  
 <213> Homo sapien

<400> 211

Met	Glu	Ser	Pro	Ser	Ala	Pro	Pro	His	Arg	Trp	Cys	Ile	Pro	Trp	Gln
1				5					10					15	
Arg	Leu	Leu	Leu	Thr	Ala	Ser	Leu	Leu	Thr	Phe	Trp	Asn	Pro	Pro	Thr
			20					25					30		
Thr	Ala	Lys	Leu	Thr	Ile	Glu	Ser	Thr	Pro	Phe	Asn	Val	Ala	Glu	Gly
	35						40					45			
Lys	Glu	Val	Leu	Leu	Leu	Val	His	Asn	Leu	Pro	Gln	His	Leu	Phe	Gly
	50					55					60				
Tyr	Ser	Trp	Tyr	Lys	Gly	Glu	Arg	Val	Asp	Gly	Asn	Arg	Gln	Ile	Ile
65					70				75						80
Gly	Tyr	Val	Ile	Gly	Thr	Gln	Gln	Ala	Thr	Pro	Gly				
			85						90						

<210> 212  
 <211> 142  
 <212> PRT  
 <213> Homo sapien

<400> 212

Glu	Lys	Gln	Lys	Asn	Lys	Glu	Phe	Ser	Gln	Thr	Leu	Glu	Asn	Glu	Lys
1				5					10					15	
Asn	Thr	Leu	Leu	Ser	Gln	Ile	Ser	Thr	Lys	Asp	Gly	Glu	Leu	Lys	Met
			20					25					30		
Leu	Gln	Glu	Glu	Val	Thr	Lys	Met	Asn	Leu	Leu	Asn	Gln	Gln	Ile	Gln
	35						40					45			
Glu	Glu	Leu	Ser	Arg	Val	Thr	Lys	Leu	Lys	Glu	Thr	Ala	Glu	Glu	Glu
	50					55					60				
Lys	Asp	Asp	Leu	Glu	Glu	Arg	Leu	Met	Asn	Gln	Leu	Ala	Glu	Leu	Asn

101

65					70					75				80	
Gly	Ser	Ile	Gly	Asn	Tyr	Cys	Gln	Asp	Val	Thr	Asp	Ala	Gln	Ile	Lys
				85					90					95	
Asn	Glu	Leu	Leu	Glu	Ser	Glu	Met	Lys	Asn	Leu	Lys	Lys	Cys	Val	Ser
			100					105					110		
Glu	Leu	Glu	Glu	Glu	Lys	Gln	Gln	Leu	Val	Lys	Glu	Lys	Thr	Lys	Val
		115					120					125			
Glu	Ser	Glu	Ile	Arg	Lys	Glu	Tyr	Leu	Glu	Lys	Ile	Gln	Gly		
	130					135					140				

&lt;210&gt; 213

&lt;211&gt; 142

&lt;212&gt; PRT

&lt;213&gt; Homo sapien

&lt;400&gt; 213

Gly	Gly	Tyr	Gly	Gly	Gly	Tyr	Gly	Gly	Val	Leu	Thr	Ala	Ser	Asp	Gly
1				5					10					15	
Leu	Leu	Ala	Gly	Asn	Glu	Lys	Leu	Thr	Met	Gln	Asn	Leu	Asn	Asp	Arg
			20					25					30		
Leu	Ala	Ser	Tyr	Leu	Asp	Lys	Val	Arg	Ala	Leu	Glu	Ala	Ala	Asn	Gly
		35					40					45			
Glu	Leu	Glu	Val	Lys	Ile	Arg	Asp	Trp	Tyr	Gln	Lys	Gln	Gly	Pro	Gly
	50					55					60				
Pro	Ser	Arg	Asp	Tyr	Ser	His	Tyr	Tyr	Thr	Thr	Ile	Gln	Asp	Leu	Arg
65					70					75					80
Asp	Lys	Ile	Leu	Gly	Ala	Thr	Ile	Glu	Asn	Ser	Arg	Ile	Val	Leu	Gln
				85				90					95		
Ile	Asp	Asn	Ala	Arg	Leu	Ala	Ala	Asp	Asp	Phe	Arg	Thr	Lys	Phe	Glu
			100					105					110		
Thr	Glu	Gln	Ala	Leu	Arg	Met	Ser	Val	Glu	Ala	Asp	Ile	Asn	Gly	Leu
		115					120					125			
Arg	Arg	Val	Leu	Asp	Glu	Leu	Thr	Leu	Ala	Arg	Thr	Asp	Leu		
	130					135					140				

&lt;210&gt; 214

&lt;211&gt; 129

&lt;212&gt; PRT

&lt;213&gt; Homo sapien

&lt;400&gt; 214

Val	Met	Arg	Val	Asp	Phe	Asn	Val	Pro	Met	Lys	Asn	Asn	Gln	Ile	Thr
1				5					10					15	
Asn	Asn	Gln	Arg	Ile	Lys	Ala	Ala	Val	Pro	Ser	Ile	Lys	Phe	Cys	Leu
			20					25					30		
Asp	Asn	Gly	Ala	Lys	Ser	Val	Val	Leu	Met	Ser	His	Leu	Gly	Arg	Pro
		35					40					45			
Asp	Gly	Val	Pro	Met	Pro	Asp	Lys	Tyr	Ser	Leu	Glu	Pro	Val	Ala	Val
	50					55					60				
Glu	Leu	Arg	Ser	Leu	Leu	Gly	Lys	Asp	Val	Leu	Phe	Leu	Lys	Asp	Cys
65					70					75					80
Val	Gly	Pro	Glu	Val	Glu	Lys	Ala	Cys	Ala	Asn	Pro	Ala	Ala	Gly	Ser
				85					90					95	
Val	Ile	Leu	Leu	Glu	Asn	Leu	Arg	Phe	His	Val	Glu	Glu	Glu	Gly	Lys
			100					105					110		

102

Gly Lys Asp Ala Ser Gly Asn Lys Val Lys Ala Glu Pro Ala Lys Ile  
 115 120 125

Glu

<210> 215  
 <211> 148  
 <212> PRT  
 <213> Homo sapien

<400> 215  
 Met Ala Thr Leu Lys Glu Lys Leu Ile Ala Pro Val Ala Glu Glu Glu  
 1 5 10 15  
 Ala Thr Val Pro Asn Asn Lys Ile Thr Val Val Gly Val Gly Gln Val  
 20 25 30  
 Gly Met Ala Cys Ala Ile Ser Ile Leu Gly Lys Ser Leu Ala Asp Glu  
 35 40 45  
 Leu Ala Leu Val Asp Val Leu Glu Asp Lys Leu Lys Gly Glu Met Met  
 50 55 60  
 Asp Leu Gln His Gly Ser Leu Phe Leu Gln Thr Pro Lys Ile Val Ala  
 65 70 75 80  
 Asp Lys Asp Tyr Ser Val Thr Ala Asn Ser Lys Ile Val Val Val Thr  
 85 90 95  
 Ala Gly Val Arg Gln Gln Glu Gly Glu Ser Arg Leu Asn Leu Val Gln  
 100 105 110  
 Arg Asn Val Asn Val Phe Lys Phe Ile Ile Pro Gln Ile Val Lys Tyr  
 115 120 125  
 Ser Pro Asp Cys Ile Ile Ile Val Val Ser Asn Pro Val Asp Ile Leu  
 130 135 140  
 Thr Tyr Val Thr  
 145

<210> 216  
 <211> 527  
 <212> PRT  
 <213> Homo sapien

<400> 216  
 Gln Arg Ala Pro Gly Ile Glu Glu Lys Ala Ala Glu Asn Gly Ala Leu  
 1 5 10 15  
 Gly Ser Pro Glu Arg Glu Glu Lys Val Leu Glu Asn Gly Glu Leu Thr  
 20 25 30  
 Pro Pro Arg Arg Glu Glu Lys Ala Leu Glu Asn Gly Glu Leu Arg Ser  
 35 40 45  
 Pro Glu Ala Gly Glu Lys Val Leu Val Asn Gly Gly Leu Thr Pro Pro  
 50 55 60  
 Lys Ser Glu Asp Lys Val Ser Glu Asn Gly Gly Leu Arg Phe Pro Arg  
 65 70 75 80  
 Asn Thr Glu Arg Pro Pro Glu Thr Gly Pro Trp Arg Ala Pro Gly Pro  
 85 90 95  
 Trp Glu Lys Thr Pro Glu Ser Trp Gly Pro Ala Pro Thr Ile Gly Glu  
 100 105 110  
 Pro Ala Pro Glu Thr Ser Leu Glu Arg Ala Pro Ala Pro Ser Ala Val  
 115 120 125  
 Val Ser Ser Arg Asn Gly Gly Glu Thr Ala Pro Gly Pro Leu Gly Pro

103

130	135	140
Ala Pro Lys Asn Gly Thr	Leu Glu Pro Gly Thr	Glu Arg Arg Ala Pro
145	150	155
Glu Thr Gly Gly Ala Pro	Arg Ala Pro Gly Ala	Gly Arg Leu Asp Leu
165	170	175
Gly Ser Gly Gly Arg Ala	Pro Val Gly Thr Gly Thr	Ala Pro Gly Gly
180	185	190
Gly Pro Gly Ser Gly Val	Asp Ala Lys Ala Gly Trp	Val Asp Asn Thr
195	200	205
Arg Pro Gln Pro Pro Pro	Pro Pro Leu Pro Pro Pro	Pro Pro Glu Ala Gln
210	215	220
Pro Arg Arg Leu Glu Pro	Ala Pro Pro Arg Ala Arg	Pro Glu Val Ala
225	230	235
Pro Glu Gly Glu Pro Gly	Ala Pro Asp Ser Arg Ala	Gly Gly Asp Thr
245	250	255
Ala Leu Ser Gly Asp Gly	Asp Pro Pro Lys Pro Glu	Arg Lys Gly Pro
260	265	270
Glu Met Pro Arg Leu Phe	Leu Asp Leu Gly Pro Pro	Gln Gly Asn Ser
275	280	285
Glu Gln Ile Lys Ala Arg	Leu Ser Arg Leu Ser Leu	Ala Leu Pro Pro
290	295	300
Leu Thr Leu Thr Pro Phe	Pro Gly Pro Gly Pro Arg	Arg Pro Pro Trp
305	310	315
Glu Gly Ala Asp Ala Gly	Ala Ala Gly Gly Glu Ala	Gly Gly Ala Gly
325	330	335
Ala Pro Gly Pro Ala Glu	Glu Asp Gly Glu Asp Glu	Asp Glu Asp Glu
340	345	350
Glu Glu Asp Glu Glu Ala	Ala Ala Pro Gly Ala Ala	Ala Gly Pro Arg
355	360	365
Gly Pro Gly Arg Ala Arg	Ala Ala Pro Val Pro Val	Val Val Ser Ser
370	375	380
Ala Asp Ala Asp Ala Ala	Arg Pro Leu Arg Gly Leu	Leu Lys Ser Pro
385	390	395
Arg Gly Ala Asp Glu Pro	Glu Asp Ser Glu Leu Glu	Arg Lys Arg Lys
405	410	415
Met Val Ser Phe His Gly	Asp Val Thr Val Tyr Leu	Phe Asp Gln Glu
420	425	430
Thr Pro Thr Asn Glu Leu	Ser Val Gln Ala Pro Pro	Glu Gly Asp Thr
435	440	445
Asp Pro Ser Thr Pro Pro	Ala Pro Pro Thr Pro Pro	His Pro Ala Thr
450	455	460
Pro Gly Asp Gly Phe Pro	Ser Asn Asp Ser Gly Phe	Gly Gly Ser Phe
465	470	475
Glu Trp Ala Glu Asp Phe	Pro Leu Leu Pro Pro Pro	Gly Pro Pro Leu
485	490	495
Cys Phe Ser Arg Phe Ser	Val Ser Pro Ala Leu Glu	Thr Pro Gly Pro
500	505	510
Pro Ala Arg Ala Pro Asp	Ala Arg Pro Ala Gly Pro	Val Glu Asn
515	520	525

&lt;210&gt; 217

&lt;211&gt; 466

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 217

gaatggtgcc	tgtcctgctg	tctctgctgc	tgttctctggg	tcttgctgtc	ccccaggaga	60
accaagatgg	tcgttactct	ctgacctata	tctacactgg	gctgtccaag	catgttgaag	120
acgtccccgc	gtttcaggcc	cttggtcac	tcaatgacct	ccagttcttt	agatacaaca	180
gtaaagacag	gaagtctcag	cccatgggac	tctggagaca	ggtggaagga	atggaggatt	240
ggaagcagga	cagccaactt	cagaaggcca	gggaggacat	ctttatggag	accctgaaag	300
acatcgtgga	gtattacaac	gacagtaacg	ggtctcacgt	attgcaggga	aggtttggtt	360
gtgagatcga	gaataacaga	agcagcggag	cattctggaa	atattactat	gatggaaagg	420
actacattga	attcaacaaa	gaaatcccag	cctgggtccc	cttcga		466

&lt;210&gt; 218

&lt;211&gt; 381

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 218

gagtttcctt	cgcaagttca	tgtggggtac	cttcccaggc	tgcctggctg	accagctggt	60
tttaaagcgc	cggggtaacc	agttggagat	ctgtgccgtg	gtcctgaggc	agttgtctcc	120
acacaagtac	tacttcctcg	tgggctacag	tgaacttttg	ctgtcctact	tttacaatatg	180
tctgtgcca	ctccacctcc	aaactgtgcc	ctcaaagggt	gtgtataagt	acctctagaa	240
caatccccctt	ttttccatca	agctgtagcc	tgcagagaat	ggaaacgtgg	gaaaggaatg	300
gtatgtgggg	gaaatgcac	ccctcagagg	actgaggcat	agtctctcat	ctgctattga	360
ataaagacct	tctatcttgt	a				381

&lt;210&gt; 219

&lt;211&gt; 1293

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 219

gaggggaggg	gcatggcggg	gatggcgctg	gcgcgggcct	ggaagcagat	gtcctgggttc	60
tactaccagt	acctgctggt	cacggcgctc	tacatgctgg	agccctggga	gcggacgggtg	120
ttcaattcca	tgctgggttc	cattgtgggg	atggcactat	acacaggata	cgtcttcatg	180
ccccagcaca	tcattggcgat	attgcactac	tttgaaatcg	tacaatgacc	aagatgcgac	240
caggatcaga	ggttccttgg	ggaagaccca	ccctacgaag	ttggaatgag	accatcagat	300
gtgataagaa	actcttctag	atgtcaacat	aaccaacctt	ataaagacta	aaattcatga	360
gtagaacagg	aaaatcatcc	tgactcatgt	gttgtgttct	ttatTTTTaa	ttttcaaaga	420
ggctcttgta	tagcagtttt	tgtctatttt	aacattgtag	tcatttgtac	tttgatatca	480
gtatTTTTctt	aacctttgtg	actgtttcaa	tattaccccc	gtgaaagctt	ttcttaatgt	540
aactttgagt	acattttaat	tgccttctat	ttttaaaact	caaaatcatt	agttgggctt	600
tactgttctt	gctattgtat	ggcatatata	tctgcctgga	tatatttcta	ctcttgacca	660
aagttttgta	aagaacaata	taagatttcg	ggtaggggta	tggggaggga	agatatttta	720
ttgagaacta	cttaacaaaa	gatttatctg	taagcttgaa	ctcaggagta	cagtttttagc	780
tatctagact	ctaacagctt	ttgctttaaa	attattaaag	tgtttcttaa	tgaaaaagaa	840
aagatcttgc	taaagttaaa	ataaggaaca	tttcaccttt	taaatattta	attcttatgt	900
ggacttatatt	ccagaaaact	ttgggtgataa	ttcttgagac	aaaagggtgg	taagtagcat	960
tattatgtaa	tgcttatata	ccatagagtt	tttaatagaa	gagaaatcca	tttcctccga	1020
gggtcactat	taacaatgta	cttccttaaa	tttagtttaa	tgattgtaat	gggtgctgca	1080
tttgcacatt	gcattaagtt	atgatgagac	gaattgttgt	taaaaattat	agcaaaaaga	1140
aatgtaaaact	tgggttaaaat	cctttcactc	tttgtattgt	tttttttaag	gttttttatc	1200
cttaaatgta	aaatgactac	ctaatttttt	gatgtaaata	cattaaattc	aaagagaaaa	1260
aaaatcaaaa	aaaaaaaaaa	aaaaaaactc	gag			1293

&lt;210&gt; 220

&lt;211&gt; 983

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 220

caggttattc	tgatcctgcc	gcctgtcttc	cctgtaagag	tggagcctcg	aggtgtacct	60
taaagtgacc	ggaatgtag	agatgcaatt	tgacagagctg	gggcaaggaa	gggctccttg	120
tcactgtagt	tactttcctt	gcagtggcca	aatgcccatt	aagaagggaat	acatgaccac	180
tgctgtgggg	agtcagcagg	tgctgtgatgc	agctggccac	actccatcca	cggccatgac	240
ataaaacaga	caagaagtaa	ggctggactg	taacacctca	aggcctgctc	cagtgaccca	300
ctttcttcag	agaggctcta	ccacacacac	aaccaccttc	caaatttaca	ctcagatcac	360
tacaccatgt	ctcccaagtt	aaaacatgta	tccacctaga	ctttaaatgt	gctttgtaac	420
tggttgatggc	actgtacaga	gggccaaagt	atttcccatc	agatagcatt	tttctgaacc	480
catgcctctt	gggacgagat	cacaggactt	gacccatcat	caaataggac	caggtgacct	540
acagagacat	cacaatgatg	gcttcctaca	gtcaagtcca	tttccaataa	tgctctcatc	600
taagagaacc	catgaacctt	atltgaatcc	tggttcaaac	aaaaacctta	aattatttat	660
gagacaatta	taaacttgat	agattttgat	gtgtgaagg	atttatgaat	atttttagtc	720
agtgatggta	tactgttaag	gaaaagggtc	atatttttagg	gacaaaggct	gaaacattta	780
tgacagagat	gatatgatat	ctgggatttg	tttttaggatg	aagtgggagg	gaggaaatga	840
atggaaatag	tgttgaaaca	gtattggcca	cgagtcagct	attgtgtgct	aagacgctcc	900
tcacaccagt	ctactctgta	tgtgtttgaa	tatctctgta	ataaacttaa	caaggaaaaa	960
aaaaaaaaaa	aaaaaaactc	gag				963

&lt;210&gt; 221

&lt;211&gt; 373

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 221

cattttatgg	gttaattttt	tattaaatag	caataagata	cttttataac	tcaataaaat	60
tattcaatga	tacattcgga	aaataaatgt	ataaaatatg	aaaaagtact	aaaaagcatt	120
tttcagtact	tttaggtaag	attaatccaa	ctaaacacta	gcatatgtta	tacagtaata	180
ataaggggaa	aatacaataa	tggttgagaaa	gcaaactcaa	agcatagatc	aatgaaaaaa	240
ttgagaaatg	gacataaatg	atttagtatt	tttaaagaga	gtgaaaaatc	attattttat	300
gctttttgtg	agcgttagat	gaattaaata	acatatgcac	atatagcttt	gcgatacaaa	360
tttccagacc	ata					373

&lt;210&gt; 222

&lt;211&gt; 544

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 222

cagagatgct	gctgctacaa	aggatcggtg	taagcagtta	acccaggaaa	tgatgacaga	60
gaaagaaaga	agcaatgtgg	ttataacaag	gatgaaagat	cgaattggaa	cattagaaaa	120
ggaacataat	gtattttcaa	acaaaataca	tgctcagttat	caagagactc	aacagatgca	180
gatgaagttt	cagcaagttc	gtgagcagat	ggaggcagag	atagctcact	tgaagcagga	240
aatgggtata	ctgagagatg	cagtcagcaa	cactacaaat	caactggaaa	gcaagcagtc	300
tgacagaacta	aataaactac	gccaggatta	tgctagggttg	gtgaatgagc	tgactgagaa	360
aacaggaaag	ctacagcaag	aggaagtcca	aaagaagaat	gctgagcaag	cagctactca	420
gttgaagggt	caactacaag	aagctgagag	aagggtggga	gaagttcaga	gctacatcag	480
gaagagaaca	gcggaacatg	aggcagcaca	gctagattta	cagagtaa	ttgtggccaa	540
agaa						544

&lt;210&gt; 223

&lt;211&gt; 316



&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 223

gaggcaaggg	atatgcttta	gtgcctatta	tagttaattc	ttcaactcca	aagtctaaaa	60
cagttgaatc	tgctgaagga	aaatctgaag	aagtaaatga	aacattagtt	ataccactg	120
aggaagcaga	aatggaagaa	agtggacgaa	gtgcaactcc	tgtaactgt	gaacagcctg	180
atatcttggg	ttcttctaca	ccaataaatg	aaggacagac	tgtgttagac	aagggtggctg	240
agcagtgtga	acctgctgaa	agtcagccag	aagcacttct	gagaggaaga	tgtttgcaag	300
gtaactctaa	cagttg					316

&lt;210&gt; 224

&lt;211&gt; 1583

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 224

cagaccacgt	ctgccctcgc	cgtcttagcc	ctgcgcccc	gcccggccgc	ggcacctccg	60
cctcgccgcc	gctaggtcgg	ccggctccgc	ccggctgccg	cctaggatga	atatcatgga	120
cttcaacgtg	aagaagctgg	cggccgacgc	aggcaccttc	ctcagtcgcg	ccgtgcagtt	180
cacagaagaa	aagcttggcc	aggctgagaa	gacagaattg	gatgctcact	tagagaacct	240
ccttagcaaa	gctgaatgta	ccaaaatatg	gacagaaaaa	ataatgaaac	aaactgaagt	300
gttattgcag	ccaaatccaa	atgccaggat	agaagaattt	gtttatgaga	aactggatag	360
aaaagctcca	agtcgtataa	acaaccacga	acttttgagg	caatatatga	ttgatgcagg	420
gactgagttt	ggcccaggaa	cagcttatgg	taatgccctt	attaaatgtg	gagaaaccca	480
aaaaagaatt	ggaacagcag	acagagaact	gattcaaacg	tcagccttaa	atcttcttac	540
tcctttaaga	aacttttatag	aaggagatta	caaaacaatt	gctaaagaaa	ggaaactatt	600
gcaaaataag	agactggatt	tggatgctgc	aaaaacgaga	ctaaaaaagg	caaaagctgc	660
agaaactaga	aattcatctg	aacaggaatt	aagaataact	caaagtgaat	ttgatcgtca	720
agcagagatt	accagacttc	tgctagaggg	aatcagcagt	acacatgccc	atcaccttcg	780
ctgtctgaat	gactttgtag	aagcccagat	gacttactat	gcacagtgtt	accagtatat	840
gttggacctc	cagaaacaac	tgggaagttt	tccatccaat	tatcttagta	acaacaatca	900
gacttctgtg	acacctgtac	catcagtttt	accaaagtcg	attggttctt	ctgccatggc	960
ttcaacaagt	ggcctagtaa	tcacctctcc	ttccaacctc	agtgacctta	aggagtgtag	1020
tggcagcaga	aaggccaggg	ttctctatga	ttatgatgca	gcaaacagta	ctgaattatc	1080
acttctggca	gatgaggtga	tcactgtgtt	cagtgttggt	ggaatggatt	cagactggct	1140
aatgggggaa	aggggaaacc	agaagggcaa	ggtgccaat	acctacttag	aactgctcaa	1200
ttaagtaggt	ggactatgga	aaggttgccc	atcatgactt	tgtatttata	tacaattaac	1260
tctaaataaa	gcagggttaag	tatcttccat	gttaatgtgt	taagagactg	aaaataaccag	1320
ccatcagaaa	ctggcctttt	tgccaataaa	gttgcatggg	aaatatattca	ttacagaatt	1380
tatgttagag	ctttcatgcc	agaatgtttt	tcttacaata	ttctcttttt	attgaggttt	1440
cactaataag	cagcttctac	ttttgagcct	caacttaaa	cagaactgtt	ttttactgga	1500
tttttcatta	acagcaagct	ttttttttta	tgtaaaataa	atctattgtg	aattgaaaaa	1560
aaaaaaaaaa	aaaaaaactc	gag				1583

&lt;210&gt; 225

&lt;211&gt; 491

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 225

gaacaacatc	atcttgaatc	actagataga	ctcttgacgg	aaagcaaagg	ggaaatgaaa	60
aaggaaaata	tgaagaaaga	tgaagcttta	aaagcattac	agaaccaagt	atctgaagaa	120
acaatcaagg	ttaggcaact	agattcagca	ttggaaattt	gtaaggaaga	acttgtcttg	180
catttgaatc	aattggaagg	aaataaggaa	aagtttgaaa	aacagttaaa	gaagaaatct	240

gaagaggtat attgtttaca gaaagagcta aagataaaaa atcacagtct tcaagagact	300
tctgagcaaa acgttattct acagcatact cttcagcaac agcagcaa at gttacaacaa	360
gagacaatta gaaatggaga gctagaagat actcaaacta aacttgaaaa acaggtgtca	420
aaactggaac aagaacttca aaaacaaagg gaaagttcag ctgaaaagtt gagaaaaatg	480
gaggagaaat g	491

<210> 226  
 <211> 483  
 <212> DNA  
 <213> Homo sapien

<400> 226						
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ggtgggaaag gacccgggac ttgaacagtg ttgtgcggcg ccatgcaggt ctccagcctc	120					
aatgaggtga agatttacag cctcagctgc ggcaagtccc ttcctgagtg gctttctgat	180					
aggaagaaga gagcgctaca gaagaaagat gtagatgtcc gtaggagaat tgaacttatt	240					
caggactttg aaatgcctac tgtgtgtacc actattaagg tgtcaaaaga tggacagtac	300					
attttagcaa ctggaacata taaacctcgg gttcgatgtt atgacaccta tcaattatcc	360					
ttgaagtttg aaaggtgttt agattcagaa gttgtcacct ttgaaatttt gtctgatgac	420					
tactcaaaga ttgtcttctt acataatgat agatacattg aatttcattc gcaatcaggt	480					
ttt	483					

<210> 227  
 <211> 486  
 <212> DNA  
 <213> Homo sapien

<400> 227						
gagcctcgct aagctccgac tctgggcggc acggggcgct ccacgatgcc gaagaacaag	60					
aagcggaaaca ctccccaccg cggtagcagt gctggcgggc gcgggtcagg agcagccgca	120					
gcgacggcgg cgacagcagg tggccagcat cgaaatgttc agccttttag tgatgaagat	180					
gcatcaattg aaacagtgag ccattgcagt gggttatagc atccttccag ttttgctgaa	240					
gatggaccag aagtccttga tgaggaagga actcaagaag acctagagta caagttgaag	300					
ggattaattg acctaacctt ggataagagt gcgaagacaa ggcaagcagc tcttgaagg	360					
attaaaaatg cactggcttc aaaaatgctg tatgaattta ttctggaaag gagaatgact	420					
ttaactgata gcattgaacg ctgcctgaaa aaaggtaaga gtgatgagca acgtgcagct	480					
gcagcg	486					

<210> 228  
 <211> 494  
 <212> DNA  
 <213> Homo sapien

<400> 228						
gaggccagga ctccgggaat gcgagcaggc cccttattct ccagtgggcc tcggtctgtc	60					
cccacagcgg cccggtcagg gttgcccag ccccaaggcg gggggcgga cccgggtgct	120					
gaaagggaca gaatgctttg acctccaagc tgttttaa at ctagtagata agccagatcc	180					
tgtgttgcca taagcccttg gccacattt aagtgggaat gcagctagct tggatgtctg	240					
aaactttgta agcgcttct gtctgaatcc tgaacacagg caccaagact actgaagaag	300					
ctcgtcattc ttgtgcaggg atagccacac aagcaaacat gtttgcaaaa cttgaaagaa	360					
agaaaattgc agaaagaaga cttgctgttc ttaagaggcc caggaagggt ctacttagga	420					
atcccaccgg cttgtgaagc aagggaatca agtttgctt caatggggaa cttgacttca	480					
ggaaaatgaa cttt	494					

<210> 229

<211> 465  
 <212> DNA  
 <213> Homo sapien

<400> 229  
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 aagcgtgggc aagattgagc actccttctg gagatccttt cacactgagc gaaagacaga 120  
 accagccaca ggcttcacgc atggtgatct gattgaaagt ttcctagata tcagccgccc 180  
 taagatgcag gaggttgtgg caaacttgca gtatgatgat ggcagtggta tgaagcggga 240  
 ggcaactgca gatgacctca tcaaagtcgt ggaggaacta actcggatcc attagccaag 300  
 gacaggatct cttttcctga ccctcctaaa ggcgttgccc tcctatcctc ccttccttgc 360  
 ccacccttgg tttctttggc atgggaaggt tttccttaac cacttgcctt agagccacca 420  
 gtgaccttgt gtggaaacag ggtttttttt acttaaaaca gttca 465

<210> 230  
 <211> 495  
 <212> DNA  
 <213> Homo sapien

<400> 230  
 caggggaaag ggtgttttggc cttgaccagc cactgctgac ctcaatctca gacctacaga 60  
 tgggtgaatat ctccctgcga gtgttgtctc gaccaatgc tcaggagctt cctagcatgt 120  
 accagcgcct agggctggac tacgaggaac gagtgttgcc gtccattgct aacgaggtgc 180  
 tcaagagtgt ggtggccaag ttcaatgcct cacagctgat caccagcggt gccaggtat 240  
 ccctgttgat ccgcccggag ctgacagaaa gggccaaagg acttcagcct catcctggat 300  
 gatgtggcca tcacagactt gagcttttagc cgagaagtac acaagctgcc tgtaagaaac 360  
 ccaaccaagt ggggtgaatt ccaaaaaccc gtgggggtga agggcttctt aagaatgcaa 420  
 ggaaggagga aaagaattcc atgggggggg ggttccttaa ccaggaaca ggggtttccc 480  
 ttgaattttt ttcca 495

<210> 231  
 <211> 498  
 <212> DNA  
 <213> Homo sapien

<400> 231  
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 ctatcgccag tcgtcggcca cgtcgtcctt cggaggcctg ggcggcggct ccgtgcgttt 120  
 tgggccgggg gtcgcttttc gcgcgccag cattcacggg ggctccggcg gccgcggcgt 180  
 atccgtgtcc tccgcccgct ttgtgtcctc gtcctcctcg gggggctacg gcggcggcta 240  
 cggcggcgct ctgaccgcgt ccgacgggct gctggcgggc aacgagaagc taaccatgca 300  
 gaacctcaac gaccgcctgc ctccctacctg gacaaagtgc gcgccttgga agcgggcaac 360  
 ggcgaaactta gaggtgaaag aatcccgcga actggtacca aaaacaaggg gcctggggcc 420  
 ttccgcgact tacagccaac ttactacacc gaacattcaa gaacttgcgg gaacaaaaat 480  
 ttttggtgcc acccattt 498

<210> 232  
 <211> 465  
 <212> DNA  
 <213> Homo sapien

<400> 232  
 cagggccggcc gagtaggaaa gctggaggcg cgggtgggga acatgtctga gtcggagctc 60  
 ggcaggaagt gggaccggtg tctggcggat gcggtcgtga agataggtagc tggtttttga 120  
 ttaggaattg ttttctcact taccttcttt aaaagaagaa tgtggccatt agccttcggt 180

109

tctggcatgg	gattaggaat	ggcttattcc	aactgtcagc	atgatttcca	ggctccatat	240
cttctacatg	gaaaatatgt	caaagagcag	gagcagtgac	ttcacctgag	aacatcccag	300
cgggaggaca	agagaaaatc	atgtttattc	ctcaggaata	cttgaagtgc	cctggagtaa	360
actgccattc	ttctgtaaca	atggtatcag	taatgcttta	aactccagca	cctgggttatg	420
catttgaaac	ccaagtctgg	ttcttggttt	ggattttctc	tctgg		465

<210> 233  
 <211> 366  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(366)  
 <223> n = A,T,C or G

<400> 233						
cagtaaaaaa	ggttatgttt	tattaattgc	tggacaaccg	tgggaaaaca	aataagcaat	60
tgacaccacc	aaattcttat	tacattcaan	ataaaanatt	tattcacacc	acaaaaagat	120
aatcacaaca	aatatacac	taacttaaaa	aacaaaagat	tatagtgaca	taaaatgtta	180
tattctcttt	ttaagtgggt	aaaagtatth	tgthttgcttc	tacataaatt	tctattcatg	240
ananaataac	aatatttaaa	atacagtgat	agthttgcatt	tcttctatag	aatgaacata	300
gacataaccc	tgaagcttht	agthttacagg	gagthttccat	gaagccacaa	actaaactaa	360
ttatca						366

<210> 234  
 <211> 379  
 <212> DNA  
 <213> Homo sapien

<400> 234						
gagggcagcc	ctcctacctg	cgcacgtggt	gccgccgctg	ctgcctcccg	ctcgccctga	60
accagtgcc	tgcagccatg	gctcccggcc	agctcgccct	atttagtgte	tctgacaaaa	120
ccggccttgt	ggaatttgca	agaaacctga	ccgctcttgg	tttgaatctg	gtcgcttccg	180
gagggactgc	aaaagctctc	agggatgctg	gtctggcagt	cacagatgtc	tctgagttga	240
cgggatttct	gaaatgttgg	ggggacgtgt	gaaaactttg	catectgcac	gatcccctgc	300
tggaatccta	gctcctaata	ttcagaagat	aatgcttgac	atgcgccaca	cttgattcaa	360
tcttataaca	attgttgcc					379

<210> 235  
 <211> 406  
 <212> DNA  
 <213> Homo sapien

<400> 235						
caggctgcac	catgtacccc	accttcagtt	taaaagaaaa	aaaaaatccc	cttcactcct	60
actgggaggt	gggaccctt	tcattttcag	ttttgctcat	ctagggaaaa	taaggctttg	120
gtttccagtt	taattgtttt	tgaccttcta	aaatgttttt	atgttagcac	tgatagttgg	180
cattactgtt	gttaagcact	gtgttccaga	ccgtgtctga	cttagtgtaa	cctaggagat	240
tttatagttt	tattttaatg	aaaccctgat	tgacgcacag	cagtggggag	aacagcgtct	300
tttacctgtc	accgaagcca	ggaagccccg	tttgtaagcg	tgtgttggtg	tgctttattg	360
tacatcctcc	agtggcgctc	tttttactct	aatgttcttt	tggttt		406

<210> 236  
 <211> 278

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 236

```
gagattagca cctgtgaaca atgcgttctc tgatgacact ctgagcatgg accaacgcct      60
tcttaagcta attctgcaaa atcacatatt gaaagtaaaa gttggcctta gcgacctcta      120
caatggacag atactggaaa ccattggagg caaacaactc cgagtctttg tgtatcggac      180
ggctatctgc atagaaaact catgcatggg gagaggaagc aagcagggaa ggaacgggtgc      240
cattcacata ttccgagaga tcatccaacc agcagaat      278
```

&lt;210&gt; 237

&lt;211&gt; 322

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 237

```
cagggccgtg gcggaggagg agcgtctgcac ggtggagcgt cgggcccacc tcacctacgc      60
ggagttcgtg cagcagtagc tgcgcccctg atcgcgaggg tcggtcctg ttcaccggcc      120
cgtctgcccc gaccgcccac ggccgccttc cctgacctc gcgcgcacgc gtggggctgg      180
ggcggcgagg ctggcggtcc ggccctggccg cgactctgcc cttctttcca gaggttccgg      240
gcctgtgtct cccgcgacag gttgctgggt tcgtttgggg acagagtggg ccggtgagca      300
ccgccaacac ctactcctac ct      322
```

&lt;210&gt; 238

&lt;211&gt; 613

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (399)

&lt;223&gt; n=A,T,C or G

&lt;400&gt; 238

```
gaattcggca ccagccttct tggatcagga ccagtctcca ccccgtttct acagtggaga      60
tcagcctcct tcttatcttg gtgcaagtgt ggataaactc catcaccctt tagaatttgc      120
agacaaatct cccacacctc ctaattttacc tagcgataaa atctaccctc cttctgggtc      180
ccccgaagag aataccagca cagccaccat gacttacatg acaactactc cagcaacagc      240
ccaaatgagc accaaggaag ccagctggga tgtggctgaa caaccacca ctgctgattt      300
tgctgctgcc acacttcagc gcacgcacag aactaatcgt ccccttcccc ctccgccttc      360
ccagagatct gcagagcagc caccagttgt ggggcaggna caagcagcaa ccaatatagg      420
attaaataat tcccacaagg ttcaaggagt agttccagtt ccagagaggc cacctgaacc      480
tcgagccatg gatgacctg cgtctgcctt catcagtgc agtggtgctg ctgctgctca      540
gtgtcccatg gctacagctg tccagccagg cctgcctgag aaagtgcggg acggtgcccc      600
ggtcccgtg ctg      613
```

&lt;210&gt; 239

&lt;211&gt; 613

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 239

```
gaattcggca ccaggggaca ctgggtgctga gctggatgat gatcagcact ggtctgacag      60
cccgtcggat gctgacagag agctgcgttt gccgtgccca gctgaggggg aagcagagct      120
```

```

ggagctgagg gtgtcgggaag atgaggagaa gctgcccgcc tcaccgaagc accaagagag 180
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tccagtccac agccccctcaa cagagggggcc ccaactccca cctgtccctg ccgccaccca 300
ggagaaatca cctgaggagc gccttttccc tgagcctttg ctccccaaag agaagcccaa 360
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cctgccagaa gctaggactc ctgtctcacc agggagcccg cagccccagc caccctgtggc 480
ggcctccacg cccccaccca gcgaggtctc cagagccttc tctctcctgt gcaaaatggc 540
aactcttaag gaaaaactca ttgcaccagt tgcggaagaa gaggcaacag ttccaaacaa 600
taagatcact gta 613

```

&lt;210&gt; 240

&lt;211&gt; 585

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 240

```

gaattcggca cgaggtgaga tctacgatga actttaagat tggaggtgtg acagaacgca 60
tgccaacccc agttattaaa gcttttggca tcttgaagcg agcggccgct gaagtaaacc 120
aggattatgg tcttgatcca aagattgcta atgcaataat gaaggcagca gatgaggtag 180
ctgaaggtaa attaaatgat cattttcctc tcgtggtatg gcagactgga tcaggaactc 240
agacaaatat gaatgtaa atgaagtcatta gcaatagagc aattgaaatg ttaggaggtg 300
aacttggcag caagatacct gtgcacccca acgatcatgt taataaaagc cagagctcaa 360
atgatacttt tcccacagca atgcacattg ctgctgcaat agaagttcat gaagtactgt 420
taccaggact acagaagtta catgatgctc ttgatgcaaa atccaaagag ttgacacaga 480
tcatcaagat tggacgtact catactcagg atgctgttcc acttactctt gggcaggaat 540
ttagtggtta tgttcaacaa gtaaaatatg caatgacaag aataa 585

```

&lt;210&gt; 241

&lt;211&gt; 566

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 241

```

gaattcggca ccaggcgagc tgcacctcga ggtgaaggcc tcactgatga acgatgactt 60
cgagaagatc aagaactggc agaaggaagc ctttcacaag cagatgatgg gcggcttcaa 120
ggagaccaag gaagctgagg acggctttcg gaaggcacag aagccctggg ccaagaagct 180
gaaagaggta gaagcagcaa agaaagccca ccatgcagcg tgcaaagagg agaagctggc 240
tatctcacga gaagccaaca gcaaggcaga cccatccctc aaccctgaac agctcaagaa 300
attgcaagac aaaatagaaa agtgcaagca agatgttctt aagaccaaag agaagtatga 360
gaagtccttg aaggaactcg accagggcac accccagtac atggagaaca tggagcaggt 420
gtttgagcag tgccagcagt tcgaggagaa acgccttcgc ttcttccggg aggttctgct 480
ggaggttcag aagcacctag acctgtccaa tgtggctggc taciaagcca ttaccatga 540
cctggagcag agcatcagag cagctg 566

```

&lt;210&gt; 242

&lt;211&gt; 556

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 242

```

gaattcggca cgagcaaagg tgaagcagga catgcctccg cccggggggct atgggcccac 60
cgactacaaa cggaacttgc cgcgtcgagg actgtcgggc tacagcatgc tggccatagg 120
gattggaacc ctgatctacg ggcactggag cataatgaag tggaaccgtg agcgcaggcg 180
cctacaaatc gaggacttcg aggctcgcac cgcgtgttg ccactgttac aggcagaaac 240
cgaccggagg accttgacga tgcttcggga gaacctggag gaggaggcca tcatcatgaa 300

```



```

ggacgtgccc gactggaagg tgggggagtc tgtgttccac acaacccgct gggtgcccc 360
cttgatcggg gagctgtacg ggctgcgcac cacagaggag gctctccatg ccagccacgg 420
cttcatgtgg tacacgtagg ccttgtgccc tccggccacc tggatccctg cccctcccca 480
ctgggacgga ataatgctc tgcagacctg gaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 540
aaaaaaaaaa ctcgag                                     556

```

&lt;210&gt; 243

&lt;211&gt; 591

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 243

```

gtctatgttt gcagaaatac agatccaaga caaagacagg atgggcaactg ctggaaaagt 60
tattaaatgc aaagcagctg tgctttggga gcagaagcaa cccttctcca ttgaggaaat 120
agaagttgcc ccaccaaaga ctaaagaagt tcgcattaag attttggcca caggaatctg 180
tcgcacagat gaccatgtga taaaagggaac aatgggtgtcc aagtttccag tgattgtggg 240
acatgaggca actgggattg tagagagcat tggagaagga gtgactacag tgaaaccagg 300
tgacaaagtc atccctctct ttctgccaca atgtagagaa tgcaatgctt gtcgcaacc 360
agatggcaac ctttgcatta ggagcgatat tactggctgt ggagtactgg ctgatggcac 420
caccagattt acatgcaagg gcaaaccagt ccaccacttc atgaacacca gtacatttac 480
cgagtacaca gtggtggatg aatcttctgt tgctaagatt gatgatgcag ctctctctga 540
gaaagtctgt ttaattggct gtgggttttc cactggatat ggcgctgctg t 591

```

&lt;210&gt; 244

&lt;211&gt; 594

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 244

```

gaattcggca cgagaacaga gtgaactgag catcagtcag aaaaagtcta tgtttgcaga 60
aatacagatc caagacaaag acaggatggg cactgctgga aaagttatta aatgcaaagc 120
agctgtgctt tgggagcaga agcaaccctt ctccattgag gaaatagaag ttgccccacc 180
aaagactaaa gaagttcgca ttaagatttt ggccacagga atctgtcgca cagatgacca 240
tgtgataaaa ggaacaatgg tgtccaagtt tccagtgtat gtgggacatg aggcaactgg 300
gattgtagag agcattggag aaggagtgtac tacagtgaac ccaggtgaca aagtcattcc 360
tctctttctg ccacaatgta gagaatgcaa tgcttgtcgc aaccagatg gcaacccttg 420
cattaggagc gatattactg gtcgtggagt actggctgat ggcaccacca gatttacatg 480
caagggcaaa ccagtcacc acttcatgaa caccagtaca tttaccgagt acacagtggg 540
ggatgaatct tctgttgcta agattgatga tgcagctcct cctgagaaag tctg 594

```

&lt;210&gt; 245

&lt;211&gt; 615

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (105)

&lt;223&gt; n=A,T,C or G

&lt;400&gt; 245

```

gtccctttcc tctgctgccg ctccgtcacg cttgtgcccg aaggaggaaa cagtgcacaga 60
cctggagact gcagttctct atccttccac agctctttca ccatnctgga tcacttcctt 120
tgaatgcaga agcttgctgg ccaaaagatg tgggaattgt tgcccttgag atctattttc 180
cttctcaata tgttgatcaa gcagagttgg aaaaatatga tgggtgtagat gctggaaagt 240

```

```

ataccattgg cttgggccag gccaatgatgg gcttctgcac agatagagaa gatattaact 300
ctctttgcat gactgtggtt cagaatctta tggagagaaa taacctttcc tatgattgca 360
ttgggcggct ggaagttgga acagagacaa tcatcgacaa atcaaagtct gtgaagacta 420
atgtgatgca gctgtttgaa gagtctggga atacagatat agaaggaatc gacacaacta 480
atgcatgcta tggaggcaca gctgctgtct tcaatgcttg ttaactggat tgagtccagc 540
tcttgggatg gacggtatgc cctggtaagt tgcaggagat attgctgtat atgccacagg 600
aaatgctaga cctac 615

```

&lt;210&gt; 246

&lt;211&gt; 546

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 246

```

gaattcggca ccaggctgcc tcccgcctgc cctgaaccca gtgcctgcag ccatggctcc 60
cggccagctc gccttattta gtgtctctgc aaaaccggcc ttgtgaattt gcaagaaacc 120
tgaccgctct tggtttgaat ctggctcgtt ccggagggac tgcaaaagct ctcagggatg 180
ctggctctggc agtcagagat gtctctgagt tgacgggatt tcctgaaatg ttggggggac 240
gtgtgaaaac tttgcatact gcagtcctat ctggaatcct agctcgtaat attccagaag 300
ataatgctga catggccaga cttgatttca atcttataag agttgttgcc tgcaatctct 360
atccctttgt aaagacagtg gcttctccag gtgtaactgt tgaggaggct gtggagcaaa 420
ttgacattgg tggagtaacc ttactgagag ctgcagccaa aaaccacgct cgagtgcagc 480
tggtgtgtga accagaggac tatgtgggtg ggtgtccacg gagatgcaga gctccgagag 540
taagga 546

```

&lt;210&gt; 247

&lt;211&gt; 564

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 247

```

gaattcggca ccagagatca cgtgcagtga gatgcagcaa aaagttgaac ttctgagata 60
tgaatctgaa aagcttcaac aggaaaattc tattttgaga aatgaaatta ctactttaaa 120
tgaagaagat agcatttcta acctgaaatt agggacatta aatggatctc aggaagaaat 180
gtggcaaaaa acggaaactg taaaacaaga aaatgctgca gttcagaaga tggttgaaaa 240
tttaaagaaa cagatttctag aattaaaaat caaaaaccaa caattggatt tggaaaatac 300
agaacttagc caaaagaact ctcaaaacca ggaaaaactg caagaactta atcaacgtct 360
aacagaaatg ctatgccaga aggaaaaaga gccaggaaac agtgcattgg aggaacggga 420
acaagagaag tttaatctga aagaagaact ggaacgttgt aaagtgcagt cctccacttt 480
agtgtcttct ctggaggcgg agctctctga agttaaaata cagacccata ttgtgcaaca 540
ggaaaaccac cttctcaaag atga 564

```

&lt;210&gt; 248

&lt;211&gt; 434

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 248

```

gttcttgttt gtggatcgct gtgatecgta cttgacaatg cagatcttcg tgaagactct 60
gactggtaag accatcacc ctcagggttg gccagtgac accatcgaga atgtcaaggc 120
aaagatccaa gataaggaag gcatccctcc tgaccagcag aggtgatctt ttgctggaaa 180
acagctggaa gatgggcgca ccctgtctga ctacaacatc cagaaagagt ccaccctgca 240
cctgggtgctc cgtctcagag gtgggatgca aatcttcgtg aagacactca ctggcaagac 300
catcaccctt gaggtggagc ccagtgacac catcgagaac gtcaaagcaa agatccagga 360
caaggaaggc attcctcctg accagcagag gttgatcttt gccggaaagc cagcctggga 420

```

agatgggggcc gccca

434

&lt;210&gt; 249

&lt;211&gt; 416

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 249

gcgggcccag	gaggcggcgg	cggcggcggc	ggacggggccc	cccgcggcag	acggcggagga	60
cggacaggac	ccgcacagca	agcacctgta	cacggccgac	atgttcacgc	acgggatcca	120
gagcgcgcgc	cacttcgtca	tggtcttcgc	gccctgggtg	ggacactgcc	agcggctgca	180
gccgacttgg	aatgacctgg	gagacaaata	caacagcatg	gaagatgcca	aagtctatgt	240
ggctaaagtg	gactgcacgg	cccactccga	cgtgtgctcc	gcccaggggg	tgcgaggata	300
ccccacctta	aagcttttca	agccaggcca	agaagctgtg	aagtaccagg	gtcctcggga	360
cttcacagaca	ctggaaaact	ggatgctgca	gacactgaac	gaggagccag	tgacac	416

&lt;210&gt; 250

&lt;211&gt; 504

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 250

gaattcggca	cgaggcgggt	aacgttatag	tatttgctcag	aagttggggg	ctccgtgggc	60
attgtgatcc	gtcccaggca	gtggattagg	aggccagaag	gagatccctt	ccacgggtgct	120
aggctgagat	ggatcctctc	agggcccaac	agctggctgc	ggagctggag	gtggagatga	180
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agctgatgaa	gaggggtgcag	cagagctctg	ggcctgcatg	aggteccctgt	cagtatacac	420
cctgggggtgt	acccaccccc	ttcccacttt	aataaacgtg	ctccctgttg	ggtgtcatct	480
gtgaagactg	ccaggcctag	ctct				504

&lt;210&gt; 251

&lt;211&gt; 607

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 251

gatgaaaata	cacaatttta	ctagcaaata	cctctactgt	aatcgctatt	taccacacaga	60
tactctgctc	aaccatatgt	taattcatgg	tctgtcttgt	ccatattgcc	gttcaacttt	120
caatgatgtg	gaaaagatgg	ccgcacacat	gcggatgggt	cacattgatg	aagagatggg	180
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ctacaaatgt	atccattgcc	ttgggtgtga	taccagcaac	atgaccgcct	caactatcac	600
tctgcat						607

&lt;210&gt; 252

&lt;211&gt; 618

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 252

```

gaattcgcac caggggtcct gctggtcttc gcctttcttc tccgcttcta ccccgtcggc 60
cgctgccact ggggtccctg gccccaccga catggcggcg gtgttgagca agtcctggag 120
cgcacggagc tgaacaagct gcccgaagtct gtccagaaca aacttgaaaa gtcccttgct 180
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gcactaactg agaaaaacaa agaacttgaa attgctcagg atcgcaatat tgccattcag 420
agccaattta caagaacaaa ggaagaatta gaagctgaga aaagagactt aattagaacc 480
aatgagagac tatctcaaga acttgaatac ttaacagagg atgttaaacy tctgaatgaa 540
aaacttaaag aaagcaatac aacaaagggt gaacttcagt taaaattgga tgaacttcaa 600
gcttctgatg tttctgtt 618

```

&lt;210&gt; 253

&lt;211&gt; 1201

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 253

```

gaattcggca ccaggggtggc gagcgcggtc gctgtgctgg ggcgagcagc ggggaccgtg 60
tgtgagtttg gcatgatttg gtccccctggg attctgcctt agcaagaaag aagttggaaa 120
tacttccttg aagaaaacta aaacaataca aaagccacag cttattgatt gcatgtcagc 180
ccccttaciaa atatggacac atttcctagc ctatttccac ctggaggaga tagtaggctg 240
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aaacataatt atcaggctct gaaaattgaa caaaaagggt tgcaggaaga atatgtaaaa 360
tcacaaaatg aacttaaacy tgtattaatt gaaaagcaag caagccagga aaaattccaa 420
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gctgagtata acaagctgcg ctacgagtat acatttctca agtcagagtt tgaacaccag 660
aaagaagagt ttactcgggt ttcagaagaa gagaaaatga aatacaagtc agaggttgca 720
cgactggaga aggacaaaga ggagctacat aaccagctgc ttagtggtga tcccacgaga 780
gacagcaaac gaatggagca acttgttcga gaaaaaacc atttgcttca gaaattgaaa 840
agtttagagg ctgaagtagc agaattaagg gctgagaaag aaaattctgg tgctcaggta 900
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ttggaggctg aaaagcagtc agctaaacta caagctgagc gtttagaaaa agaactacia 1020
tcaagcaatg aacagaatac ctgcttaatc agcaaactgc atagagctga ccgagaaatc 1080
agcacactgg ccagtgaagt gaaagagctt aaacatgcaa acaaactaga aataactgac 1140
atcaaactgg aggcagcaag agctaagagt gagctcgaaa gagaaaggaa taagatccaa 1200
a 1201

```

&lt;210&gt; 254

&lt;211&gt; 560

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 254

```

gaattcggca ccagtttggg gggtagaggt taattggaaa tggctctctg ggactgaaaa 60
ctgatgtttt tgcagattac ctgagggaaa cggaggtttg ttgagttaca gacacattaa 120
accaaaaggc gtgggaaaac ccctctccag ctccagggga ttggtcagga ccaccacta 180
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ttttgatggg aaattgccat gaccacaggg gtttgaggtt ctgctttttt tttttcttct 300
tctttttctg gggactgggg gactcctccc aagatcacat ttagcatct ttctctccta 360
ctccatttag aaaaataagt aacaggtgaa atgtggtctc agtgttaacg ggataattct 420
gctaccggct cctccctgat gattctgaaa tacactactg aacgagctct ggctggctct 480

```

ttctatcctg gatgtggttc ttctgtgtag caattccttg atgtccagtt tggaaagatg 540  
tactcttctc aacaagaaaa 560

<210> 255  
<211> 612  
<212> DNA  
<213> Homo sapiens

<400> 255  
gaattcggca ccaggcgggg cagcagggcc gcggccatgg ggagcttgaa ggaggagctg 60  
ctcaaagcca tctggcacgc cttcaccgac tccaccagga ccacagggca aggtctccaa 120  
gtcccagctc aaggtccttt ccataacct gtgcacgggt ctgaagggtc ctcatgaccc 180  
agttgccctt gaagagcact tcagggatga tgatgagggt ccagtgtcca accagggtta 240  
catgccttat ttaaacagggt tcatttttga aaagggtccaa gacaactttg acaagattga 300  
attcaatagg atgtgttgga ccctctgtgt caaaaaaaaa cctcacaag aatcccctgc 360  
tcattacaga agaagatgca tttaaaatat gggttatttt caacttttta tctgaggaca 420  
agtatccatt aattattgtg tcagaagaga ttgaatacct gcttaagaag cttacagaag 480  
ctatgggagg aggttggcag caagaacaat ttgaacatta taaaatcaac tttgatgaca 540  
gtaaaaatgg cctttctgca tgggaactta ttgagcttat tggaaatgga cagtttagca 600  
aaggcatgga cc 612

<210> 256  
<211> 1132  
<212> DNA  
<213> Homo sapiens

<400> 256  
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cacatgatga aactcagcat caagggtgtg ctccagtcgg ctctgagcct gggccgcagc 180  
ctggatgcgg accatgcccc cttgcagcag ttctttgtag tgatggagca ctgcctcaaa 240  
catgggctga aagttaagaa gagttttatt ggccaaaata aatcattctt tggtectttg 300  
gagctggtgg agaaactttg tccagaagca tcagatatag cgactagtgt cagaaatctt 360  
ccagaattaa agacagctgt gggaagaggc cgagcgtggc tttatcttgc actcatgcaa 420  
aagaaactgg cagattatct gaaagtgtt atagacaata aacatctctt aagcgagtgc 480  
tatgagcctg aggccttaat gatggaggaa gaagggatgg tgattgttgg tctgctggtg 540  
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ggagtaatag atttttccct ctaccttaag gatgtgcagg atcttgatgg tggcaaggag 660  
catgaaagaa ttactgatgt ccttgatcaa aaaaattatg tggaagaact taaccggcac 720  
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gaaaaagaac tggagttaca aattggaatg aaaaccgaaa tggaaattgc aatgaagtta 1080  
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<210> 257  
<211> 519  
<212> DNA  
<213> Homo sapiens

<400> 257  
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```

ccccggccggg cccatcctct ccatccgggt ctgcagggac atgatcacc cccgctcctt 180
gggctacgcg tacgtgaact tccagcagcc ggcggacgcg gaacgtgctt tggacaccat 240
gaattttgat gttataaagg gcaagccagt acgcatcatg tggctctcagc gtgatccatc 300
acttcgcaaa agtggagtāg gcaacatatt cattaaaaat ttggacaaat ccatcgacaa 360
taaagcacta tatgatacgt tttctgcgtt tggtaacatc ctttcatgta aggtggtttg 420
tgatgaaaat ggctccaagg gctatggatt tgtacacttt gaaacacagg aagcagctga 480
aagagctatt gaaaaaatga atgggatgct tctaaatga 519

```

&lt;210&gt; 258

&lt;211&gt; 596

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 258

```

gctttgccaa agacttagaa gctaagcaga aaatgagctt aacatcctgg tttttggtga 60
gcagtggagg cactcgccac aggctgccac gagaaatgat ttttggttga agagatgact 120
gtgagctcat gttgcagtct cgtagtgtgg ataagcaaca cgctgtcatc aactatgatg 180
cgtctacgga tgagcattta gtgaaggatt tgggcagcct caatgggact tttgtgaatg 240
atgtaaggat tccggaacag acttatatca ccttgaaact tgaagataag ctgagatttg 300
gatatgatac aaatcttttc actgtagtac aaggagaaat gagggtcctt gaagaagctc 360
ttaagcatga gaagtttacc attcagcttc agttgtccca aaaatcttca gaatcagaat 420
tateccaaatc tgcaagtgcc aaaagcatag attcaaagggt agcagacgct gctactgaag 480
tgcagcacaa aactactgaa gcactgaaat ccgaggaaaa agccatggat atttctgcta 540
tgccccgtgg tactccatta tatgggcagc cgtcatggtg gggggatgat gaggtg 596

```

&lt;210&gt; 259

&lt;211&gt; 595

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 259

```

gaattcggca ccagagaaaa agcttcaagg tatattgagt cagagtcaag ataaatcact 60
tcggagaatt tcagaattaa gagaggagct gcaaattggac cagcaagcaa agaaacatct 120
tcaggacgag tttgatgcat gtttgaggga gaaagatcag tatatcagtg ttctccagac 180
tcaggtttct cttctaaagc agcgattaca gaatggccca atgaatgttg atgctcccaa 240
accctccct cccggggagc tccaggcaga agtgcacggt gacacggaga agatggaggg 300
cgtcggggaa ccagtgggag gtgggacttc cgctaaaacc ctggaaatgc tccagcaaag 360
agtgaacgt caggagaatc tgcttcagcg ctgtaaggag acaattgggt cccacaagga 420
gcagtgcgca ctgctgctga gtgagaagga ggcactgcag gagcagttgg atgaaaggct 480
gcaggagctg gaaaagatga aggggatggt aataaccgag acgaagcggc aaatgcttga 540
gaccctggaa ctgaaagaag atgaaattgc tcagcttcgt agtcatatca aacag 595

```

&lt;210&gt; 260

&lt;211&gt; 994

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 260

```

gaattcggca cgaggcgttg cctgccttct tgctgtctat cagcctttct tgctcttcc 60
ttttcgctt cctgttctt ccttttctca aacaaacaag acatggcaaa ccgcagtcta 120
accagccct ttgaaattat ccatagtttt acagacagct ccaggccatg agccacaatg 180
tccaaaatta ttcttgagca ctgatataaa ttacttagac cttctttgag ggcagaactc 240
agctgttgct ctcatgatgg gcagtgctgg aaagggttct ggtatgtctt caaaatgagt 300
ccacgagttt actgagtgtc tacaggtaaa ggaatgaata taagatgtct ttctgatcag 360
aacagggtgc ccttcacatg agctttacta gactctggga gggaaaagta gccaaagtact 420

```



```

tctgaacccat tttttaatac ttgtttttgtc atgggtgaaat tatagcagtt atcccaaaat 480
gttttaatta tcaaaataact gtctttttaa aaaaaaaaaa agtaacacct tttaaagcat 540
tagatttcac ttgggtttct tttccaaaaa atgctaggta gacaaggcat tgtaaaccatg 600
agtttccttt aagaaccatc agaataataa tttaacatga agaaaactgc tatatctagt 660
agaaataata tctaaagttt aacaactaaa gtaccctcac agaatagcaa atacccttct 720
gttctggaca tgggttcaaa tttgaatatg gaaataattt ccttggaagt ccctagaggc 780
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tgcagattta tgccttattt tttagcattt tttaaatgtt gggctcttca aggtgttttt 900
tgctttttat tagatctata taaataagtt aactagcaat ttagttttgt atttaagcta 960
cacttaatct ttttctttgg tgatatttat ttct 994

```

&lt;210&gt; 261

&lt;211&gt; 594

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (538)

&lt;223&gt; n=A,T,C or G

&lt;400&gt; 261

```

gaattcggca ccagtggaga tccagctgaa ccatgccaac cgccaggctg cggaggcaat 60
caggaacctt cggaacaccc aggggaatgct gaaggacaca cagctgcacc tggacgatgc 120
tctcagaggc caggacgacc tgaaagagca gctggccatg gttgagcgca gagccaacct 180
gatgcaggct gagatcgagg agctcagggc atccctggaa cagacagaga ggagcaggag 240
agtggccgag caagagctac tggatgccag tgagcgcgctg cagctcctcc acaccagaa 300
caccagcctc atcaacacca agaagaagct ggagacagac atttcccaa tccagggaga 360
gatggaagac atcgtccagg aagcccgcga cgagaagag aaggccaaga aagccatcac 420
tgatgccgcc atgatggcgg aggagctgaa gaaggagcag gacaccagcg cccacctgga 480
gcggatgaag aagaacatgg agcagaccgt gaaggacctg cagcaccgtc tggacgangc 540
tgagcagctt ggcgctgaag ggcgggcaag aagcagatcc agaaactgga ggct 594

```

&lt;210&gt; 262

&lt;211&gt; 594

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 262

```

gaaaagggtgg ctggagccaa aggcatagtc agggttaatg ctcttttttc tttatcccaa 60
atcagatagt gtttaggctt tttcatcaaa tataaaaacc cagcccagtt catggctcat 120
tcggcagcaa ccctgagacg ctttacagct ctagacccta aaagggtcaa aggccgtctt 180
atgctcaata tacattttat taccatctt gccccggaca ttaaataaaa ctccaaaaat 240
taaataccggc cctcaaacc cacaacagga cttaattgac ctacacctca aggtgtagaa 300
taataaaaaa aaaaagttgc aattccttgc ctccgctgtg agacaaacc cagccacatc 360
tccagcacac aagaacttcc aaacgcctga accacagcag ccaggcgctt ctccagaacc 420
tcctcccccga ggagcttgct acatgtgccg gaaatctggc cactaggcca aggaatgcct 480
gcagccccgg attcctccta agccgtgtcc catctgtgcg ggacccact gaaaatcgga 540
ctgttcaact cacctggcag ccactctcag agaccctgga actctggccc aagg 594

```

&lt;210&gt; 263

&lt;211&gt; 506

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 263

```

gaattcggca cgagcggaaa cttagggggcc acgtgagcca cggccacggc cgcataaggca 60
agcaccggaa gcaccccggc ggccgcggta atgctggtgg tctgcatcac caccggatca 120
acttcgacaa ataccacca ggctactttg ggaaagtggg tatgaagcat taccacttaa 180
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tgcgatcggg ctactataaa gttctgggaa agggaaagct cccaaagcag cctgtcatcg 360
tgaaggccaa attcttcagc agaagagctg aggagaagat taagagtgtt gggggggcct 420
gtgtcctggg ggcttgaagc cacatggagg gagtttcatt aaatgctaac tactttttaa 480
aaaaaaaaa aaaaaaaaaa ctcgag                                     506

```

&lt;210&gt; 264

&lt;211&gt; 600

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (32)

&lt;223&gt; n=A,T,C or G

&lt;400&gt; 264

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ggctcgtgaa cacacactga cagctatagg gnaggcggcg gcaccgtccc cgcttcccct 60
cggcggcggg gtgtcccgtc ggccggccctg aagtgaccca taaacatgtc ttgtgagagg 120
aaaggcctct cggagctgcg atcggagctc tacttctca tcgcccgggt cctggaagat 180
ggaccctgtc agcaggcggc tcaggtgctg atccgcgagg tggccgagaa ggagctgctg 240
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cagtctttac tacgcacaaa taaaagctgc aagcatgttg tgtggaaagg atctgctctg 480
gctgcgttgc actgtggaag accacctgag tcaccagtta actatggtag cccaccagc 540
attgcggata ctctgttttc aaggaagctg aatgggaaat acagacttga gcgacttggt 600

```

&lt;210&gt; 265

&lt;211&gt; 534

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 265

```

gaattcggca cgagtgagga gcccatactg gcgacgcccc ctaagcggcg ggcggtggag 60
gccacggggg agaaagtgtc gcgctacgag accttcatca gtgacgtgct gcagcgggac 120
ttgcgaaagg tgctggacca tcgagacaag gtatatgagc agctggccaa ataccttcaa 180
ctgagaaatg tcattgagcg actccaggaa gctaagcact cggagttata tatgcaggtg 240
gatttgggct gtaacttctt cgttgacaca gtggtcccag atacttcacg catctatgtg 300
gccctgggat atgggttttt cctggagttg acactggcag aagctctcaa gttcattgat 360
cgtaagagct ctctcctcac agagctcagc aacagcctca ccaaggactc catgaatatc 420
aaagcccata tccacatgtt gctagagggg cttagagaac tacaaggcct gcagaatttc 480
ccagagaagc ctcaccattg acttcttccc cccatcctca gacattaaag agcc                                     534

```

&lt;210&gt; 266

&lt;211&gt; 552

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 266

120

```

gaattcggca ccagggcacc tccgcctcgc cgccgctagg tcggccggct ccgcccggct 60
gccgcctagg atgaatatca tggacttcaa cgtgaagaag ctggcggccg acgcaggcac 120
cttcctcagt cgcgccgtgc agttcacaga agaaaagctt ggccaggctg agaagacaga 180
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aaaaataatg aaacaaactg aagtgttatt gcagccaaat ccaaagtcca ggatagaaga 300
at ttgtttat gagaaactgg atagaaaagc tccaagtcgt ataaacaacc cagaactttt 360
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ccttattaaa tgtggagaaa cccaaaaaag aattggaaca gcagacagag aactgattca 480
aacgtcagcc ttaaattttc ttactccttt aagaaacttt atagaaggag attacaaaac 540
aattgctaaa ga 552

```

&lt;210&gt; 267

&lt;211&gt; 551

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 267

```

gaagcctacc agccagggtgc cggccccccc acccccggcc cagccccctc ctgcagcggt 60
ggaagcggct cggcagatcg agcgtgaggc ccagcagcag cagcacctgt accgggtgaa 120
catcaacaac agcatgcccc caggacgcac gggcatgggg accccgggga gccagatggc 180
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gccagctcc cctcagcagc aacagcaggt gctgaacatt ctcaaataca acccgcagct 480
aatggcagct ttcatacaac agcgcacagc caagtacgtg gccaatcagc ccggcatgca 540
gccccagcct g 551

```

&lt;210&gt; 268

&lt;211&gt; 573

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 268

```

gaattcggca ccaggggttcc ttgtgggcta gaagaatcct gcaaaaatgt ctctctatcc 60
atctctcgaa gacttgaagg tagacaaagt aattcaggct caaactgctt tttctgcaaa 120
ccctgccaat ccagcaattt tgtcagaagc ttctgctcct atccctcacg atggaaatct 180
ctateccaga ctgtatccag agctctctca atacatgggg ctgagtttaa atgaagaaga 240
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tccagcctca ttggttggtc tgagatttgg ggaccaagta cttcagatca atggtgaaaa 540
ctgtgcagga tggagctctg ataaagcgca caa 573

```

&lt;210&gt; 269

&lt;211&gt; 500

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 269

```

gaatcggcac caggaaacct ttattagcag agatagctgg cttggatcag attacgggga 60
atgtggggga gccatgaaga aactaactaa aggggagcct ttggggacca gggggagaca 120
agtcactatt ttgagggaga aagctctgga ttgattctga caggacactt gagtgtgaac 180
tgtccaagct aagcctctgg gtgtgtagag agagccctta cagatagata gcacctttgc 240

```

tttcagagtg gaaggactag ccactaagga ccagaccaag atgcatgtag gtcactgaca 300  
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aatttcctaa aagccataat ccagcaagct gaactcatga gaagggtctgc ttcattgttga 420  
gcatggaaga cagaacacag acggaaactg cagtgatggg gtgaagacac cacggatagg 480  
ttaggggcag tgaggaggaa 500

<210> 270

<211> 224

<212> DNA

<213> Homo sapiens

<400> 270

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tggtcgtgat ccttgcatct gttacttagg gtcaaggctt gggctcttgcc ccgcagaccc 180  
ttgggacgac ccggccccag cgcagctatg aacctggagc gagg 224

<210> 271

<211> 447

<212> DNA

<213> Homo sapiens

<400> 271

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cggcgccatg aagggcaagg aggagaagga gggcggcgca cggctgggcg ctggcgggcg 180  
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gggtggccgtg tattacacca accgggcctt gtgctacctg aagatgcagc agcacgagca 360  
ggccctggcc gactgccggc gcgccttgga gctggacggg cagtctgtga aggcgcactt 420  
cttcctgggg cagtgccagc tggagat 447

<210> 272

<211> 606

<212> DNA

<213> Homo sapiens

<400> 272

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aaactgaaga ccgaaactga caaagaaaat gctgaagtga agtttaaaga ttttcttctg 180  
tccttgaaga ctatgatgtt ttctgaagat gaggctcttt gtgttgtaga cttgctaaag 240  
gagaagtctg gtgtaataca agatgcttta aagaagtcaa gtaagggaga attgactacg 300  
cttatacatc agcttcaaga aaaggacaag ttactcgctg ctgtgaaggga agatgctgct 360  
gctacaaagg atcgggtgta gcagttaacc caggaaatga tgacagagaa agaaagaagc 420  
aatgtgggta taacaaggat gaaagatcga attggaacat tagaaaagga acataatgta 480  
tttcaaaaca aaatacatgt cagttatcaa gagactcaac agatgcagat gaagtttcag 540  
caagttcgtg agcagatgga ggcagagata gctcacttga agcaggaaaa tgggtatact 600  
ggagaa 606

<210> 273

<211> 598

<212> DNA

<213> Homo sapiens

&lt;400&gt; 273

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ccgcctcagc	tgtcgcctct	gtgggtcggt	cctctccggc	acttgggctc	cagtcgcgcc	120
ctccaagccc	ttcaggccgc	cccagtgtcc	tcctccttct	ccggccagac	ccagccccgc	180
gaagatggtg	gaccgcgagc	aactgggtgca	gaaagccccg	ctggccgagc	aggcggagcg	240
ctacgacgac	atggccgcgg	ccatgaagaa	cgtgacagag	ctgaatgagc	cactgtcgaa	300
tgaggaacga	aaccttctgt	ctgtggccta	caagaacgtt	gtggggggcac	gccgctcttc	360
ctggagggtc	atcagtagca	ttgagcagaa	gacatctgca	gacggcaatg	agaagaagat	420
tgagatggtc	cgtgcgtacc	gggagaagat	agagaaggag	ttggaggctg	tgtgccagga	480
tgtgctgagc	ctgctggata	actacctgat	caagaattgc	agcgagaccc	agtacgagag	540
caaagtgttc	tacctgaaga	tgaaagggga	ctactaccgc	tacctggctg	aagtggcc	598

&lt;210&gt; 274

&lt;211&gt; 536

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 274

gcaccaagag	actaaacaag	aaagtggatc	agggagaag	aaagcttcat	caaagaaaca	60
aaagacagaa	aatgtcttcg	tagatgaacc	ccttattcat	gcaactactt	atattccttt	120
gatggataat	gctgactcaa	gtcctgtggt	agataagaga	gaggttattg	atttgcttaa	180
acctgaccaa	gtagaaggga	tccagaaatc	tgggactaaa	aaactgaaga	ccgaaactga	240
caaagaaaat	gctgaagtga	agtttaaaga	ttttcttctg	tccttgaaga	ctatgatgtt	300
ttctgaagat	gaggctcttt	gtgttgtaga	cttgctaaag	gagaagtctg	gtgtaataca	360
agatgcttta	aagaagtcaa	gtaagggaga	attgactacg	cttatacatc	agcttcaaga	420
aaaggacaag	ttactcgctg	ctgtgaagga	agatgctgct	gctacaaagg	atcggtgtaa	480
gcagttaacc	caggaaatga	tgacagagaa	agaaagaagc	aatgtgggta	taacaa	536

&lt;210&gt; 275

&lt;211&gt; 494

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (379)

&lt;223&gt; n=A,T,C or G

&lt;400&gt; 275

gaattcggca	ccagggtcgc	ggttcttggt	tgtggatcgc	tgtgatcgtc	acttgacaat	60
gcagatcttc	gtgaagactc	tgactggtaa	gaccatcacc	ctcgagggtg	agcccagtga	120
caccatcgag	aatgtcaagg	caaagatcca	agataaggaa	ggcatccctc	ctgaccagca	180
gaggctgac	tttgctggaa	aacagctgga	agatgggcgc	accctgtctg	actacaacat	240
ccagaaagag	tccaccctgc	acctgggtgct	ccgtctcaga	ggtagggatgc	aaatcttcgt	300
gaagacactc	actggcaaga	ccatcaccct	tgagggtggag	cccagtgaca	ccatcgagaa	360
cgtcaaagca	aagatccang	acaaggaagg	cattcctcct	gaccagcaga	ggttgatctt	420
tgccggaaag	cagctggaag	atgggcgcac	cctgtctgac	tacaacatcc	agaaagagtc	480
taccctgcac	ctgg					494

&lt;210&gt; 276

&lt;211&gt; 484

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 276

```

ggctttttaac cagaagtcaa acctgttcag acagaaggca gtcacagcag aaaaatcttc 60
agacaaaagg cagtcacagg tgtgcaggga gtgtgggcga ggcttttagca ggaagtcaca 120
gctcatcata caccagagga cacacacagg agaaaagcct tatgtctgcg gagagtgtgg 180
gcgaggcctt atagttgagt cagtcctccg caaccacctg agtacacact ccggggagaa 240
accttatgtg tgcagccatt gtgggcgagg ctttagctgc aagccatacc tcatcagaca 300
tcagaggaca cacacaaggg agaaatcggt tatgtgcaca gtgtgtgggc gaggctttcg 360
tgaaaagtca gagctcatta agcaccagag aattcacacg ggggataagc cttatgtgtg 420
cagagattga ggccgaggct ttgtaaagga gatcatgtct caacacacac cagaggatta 480
catt 484

```

&lt;210&gt; 277

&lt;211&gt; 513

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 277

```

gcttgaggct gccaatcaga gcttggcaga gctgagagat cagcggcagg gggagcgcct 60
ggaacatgca gcagctttgc gggccctaca agatcaggta tccatccaga gtgcagatgc 120
acaggaacaa gtggaagggc ttttggtgta gaacaatgcc ttgaggacta gcctggctgc 180
cctggagcag atccaaacag caaagaccca agaactgaat atgctccggg aacagaccac 240
tgggctggca gctgagttgc agcagcagca ggctgagtag gaggacctta tgggacagaa 300
agatgacctc aactcccagc tccaggagtc attacggggc aatagtcgac tgctggaaca 360
acttcaagaa atagggcagg agaaggagca gttgacctag gaattacagg aggtcggaa 420
gagtgcggag aagcgggaagg ccatgcttgg atgagctagc aatggaaacg ctgcaagaga 480
agtcccacac aaggaagagc ttgggagcag ttc 513

```

&lt;210&gt; 278

&lt;211&gt; 471

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 278

```

gaattcggca ccagccaagg ccctgtccct ggctcggggc cttgaagagg ccttggaagc 60
caaagaggaa ctcgagcgga ccaacaaaat gctcaaagcc gaaatggaag acctgggtcag 120
ctccaaggat gacgtgggca agaacgtcca tgagctggag aagtccaagc gggccctgga 180
gacctcagat gaggagatga agacgcagct ggaagagctg gaggacgagc tgcaagccac 240
ggaggacgcc aaactgcggc tggaagtcaa catgcaggcg ctcaagggcc agttcgaaag 300
ggatctccaa gcccgggacg agcagaatga ggagaagagg aggcaactgc agagacagct 360
tcacgagtat gagacggaac tggaagacga gcgaaagcaa cgtgccctgg cagctgcagc 420
aaagaagaag ctggaagggg acctgaaaga cctggagctt caggccgact t 471

```

&lt;210&gt; 279

&lt;211&gt; 497

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (457)

&lt;223&gt; n=A,T,C or G

&lt;221&gt; misc\_feature

&lt;222&gt; (471)

&lt;223&gt; n=A,T,C or G

&lt;400&gt; 279



124

```

gaattcggca cgaggccaca gaggcggcgg agagatggcc ttcagcgggtt cccaggctcc 60
ctacctgagt ccagctgtcc ccttttctgg gactattcaa ggaggtctcc aggacggact 120
tcagatcact gtcaatggga ccgttctcag ctccagtggg accaggtttg ctgtgaactt 180
tcagactggc ttcagtggaa atgacattgc ctccacttc aaccctcggg ttgaagatgg 240
aggggtacgtg gtgtgcaaca cgaggcagaa cggaagctgg gggcccagg agaggaagac 300
acacatgcct ttccagaagg ggatgccctt tgacctctgc ttcttggtgc agagctcaga 360
tttcaagggtg atggtgaacg ggatcctctt cgtgcagtac ttccaccgcg tgcccttcca 420
ccgtgtggac accatctccg tcaatggctc tgtgcanctg tctacatca ncttccagac 480
ccagacagtc atccaca 497

```

&lt;210&gt; 280

&lt;211&gt; 544

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (451)

&lt;223&gt; n=A,T,C or G

&lt;400&gt; 280

```

gaattcggca ccagaatagg aacagctccg gtctacagct cccagcgtga ggcacgcaga 60
agacgggtga tttctgcatt tccatctgag gtaccgggtt catctcacta gggagtggca 120
gacagtgggc gcaggccagt gtgtgtgctc accgtgcgcg agccgaagca gggcgaggca 180
ttgcctcacc tgggaagcac aaggggtcag ggagttccct ttccgagtca aagaaagggg 240
tgacggacgc acctggaaaa tcgggtcact cccacccgaa tattgtgctt ttcagaccgg 300
cttaagaaac ggcgcaccac gagactatat cccacacctg gctcagaggg tctacgccc 360
acggaatctc gctgattgct agcacagcag tcttagatca aactgcaagg ggggcaacga 420
ggctggggga ggggcgcccg ccattgccc ngcttgctta ggtaaacaaa gcagccggga 480
agcttgaact ggggtggagcc caccacagct caaggaggcc tgctgcctc tgragctcca 540
cctc 544

```

&lt;210&gt; 281

&lt;211&gt; 527

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (456)

&lt;223&gt; n=A,T,C or G

&lt;400&gt; 281

```

gaattcggca cgaggcctcg ctcagctcca acatggcaaa aatctccagc cctacagaga 60
ctgagcgggtg catcgagtcc ctgattgctg tcttccagaa gtatgctgga aaggatgggt 120
ataactacac tcttccaag acagagttcc taagcttcat gaatacagaa ctagctgcct 180
tcacaaagaa ccagaaggac cctgggtgtc ttgaccgcat gatgaagaaa ctggacacca 240
acagtgatgg tcagctagat ttctcagaat ttcttaatct gattggtggc ctagctatgg 300
cttgccatga ctcttctc aaggctgtcc ctccccagaa gcggacctga ggacccttg 360
gccctggcct tcaaaccac ccccttctc tccagccttt ctgtcatcat ctccacagcc 420
caccatccc ctgagcacac taaccacctc atgcanggcc ccctgccaa tagtaataaa 480
gcaatgtcct tttttaaaac atgaaaaaaa aaaaaaaaaa actcgag 527

```

&lt;210&gt; 282

&lt;211&gt; 514

<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (494)  
<223> n=A,T,C or G

<400> 282  
ggaagactgg agcctttgcg gcggcgctgc ccctcccctg gtccccgcga gctcggaggg 60  
cccggctggt gctgcggggg ccccgaggagg ttgaaaacta agcatgggga agagctgcaa 120  
ggtggtcgtg tgtggccagg cgtctgtggg caaaacttca atcctggagc agcttctgta 180  
tgggaaccat gtagtgggtt cggagatgat cgagacgcag gaggacatct acgtgggctc 240  
cattgagaca gaccgggggg tgcgagagca ggtgcgtttc tatgacaccc gggggctccg 300  
agatggggcc gaactgcccc gacactgctt ctcttgcact gatggctacg tcctgggtcta 360  
tagcacagat agcagagagt cttttcagcg tgtggagctg ctcaagaagg agattgacaa 420  
atccaaggac aagaaggagg tcaccatcgt ggtccttggc aacaagtgtg acttacagga 480  
gcagcggcgt gtanacccaa atgtggctca acac 514

<210> 283  
<211> 484  
<212> DNA  
<213> Homo sapiens

<400> 283  
gggcgggcgg tggacagtca tggcggcccg gcgcggggct ctcatagtgc tggagggcgt 60  
ggaccgcgcc gggaagagca cgcagagccg caagctggtg gaagcgtgtg gcgcgcgggg 120  
ccaccgcgcc gaactgctcc ggttcccggg aagatcaact gaaatcggca aacttctgag 180  
ttcctacttg caaaagaaaa gtgacgtgga ggatcactcg gtgcacctgc ttttttctgc 240  
aaatcgctgg gaacaagtgc cgttaattaa ggaaaagttg agccagggcg tgaccctcgt 300  
cgtggacaga tacgcatttt ctggtgtggc cttcaccggt gccaaaggaga atttttccct 360  
agactggtgt aaacagccag acgtgggcct tcccaaaccg gacctggtcc tgttcctcca 420  
gttacagctg gcggatgctg ccaagcgggg agcgtttggc catgagcgct atgagaacgg 480  
ggct 484

<210> 284  
<211> 514  
<212> DNA  
<213> Homo sapiens

<400> 284  
gaattcggca cgaggcggag gccgcggagg ctctcgggtc cttcagcacc cctcggccccg 60  
acgcacccac gcccctcacc ccccgagagc cgaaaatgga cccaagtggg gtcaaagtgc 120  
tggaaacagc agaggacatc caggagaggc ggcagcaggt cctagaccga taccaccgct 180  
tcaaggaact ctcaaccctt aggcgtcaga agctggaaga ttcctatcga ttccagttct 240  
ttcaaagaga tgctgaagag ctggagaaat ggatacagga aaaacttcag attgcatctg 300  
atgagaatta taaagaccca accaacttgc agggaaagct tcagaagcat caagcatttg 360  
aagctgaagt gcaggccaac tcaggagcca ttgttaagct ggatgaaact ggaaacctga 420  
tgatctcaga agggcatttt gcatctgaaa ccatacggac ccgtttgatg gagctgcacc 480  
gccagtggga attacttttg gagaagatgc gaga 514

<210> 285  
<211> 383  
<212> DNA  
<213> Homo sapiens

&lt;400&gt; 285

```

gaattcggca cgaggccggg ctccaccgcg catcctgctc cactctggcg accgcccccg 60
gggcccccg cgcgggcgcg gcgcccgcga tgggagagga ggactactat ctggagctgt 120
gcgagcgggc ggtgcagttc gagaaggcga accctgtcaa ctgcgtcttc ttcgatgagg 180
ccaacaagca ggtttttgct gttcgatctg gtggagctac tggcgtggta gttaaaggcc 240
cagatgatag gaatcccatc tcatttagaa tggatgacaa aggagaagtg aagtgcatta 300
agttttcctt agaaaataag atattggctg ttcagaggac ctcaaagact gtggattttt 360
gtaattttat ccctgataat tcc                                     383

```

&lt;210&gt; 286

&lt;211&gt; 943

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 286

```

gaattcggca ccagggccgt ggcgaggag gagcgctgca cggtggagcg tcgggcccgc 60
ctcacctacg cggagtctgt gcagcagtac gtgcgcccct gatcgcgag gtcgcgtcct 120
gttcaccggc ccgtctgccc cgaccgcccaggccgcctt cccctgacct cgcgcgcacg 180
cgtggggctg gggcgggcag gctggcggtc cgccctggcc gcgactctgc ccttctttcc 240
agaggttccg ggccctgtgc tcccgcgaca ggttgctggc ttcgtttggg gacagagtgg 300
tccggctgag caccgccaac acctactcct accacaaagt ggacttgccc ttccaggagt 360
atgtggagca gctgctgcac cccagggacc ccacctccct gggcaatggg gaggcagccc 420
taggcggcgg tagggggtgg ggacgcttgg agtctccagg tgccaggatc cctgtccccg 480
ccgtctctgt tggcagacac cctgtacttc ttcggggaca acaacttcac cgagtggggc 540
tctctcttcc ggcactactc cccacccccca tttggcctgc tgggaaccgc tccagcttac 600
agctttggaa tcgcaggagc tggctcgggg gtgcccttcc actggcatgg acccgggtac 660
tcagaagtga tctacggtcg taagcgctgg ttcctttacc cacctgagaa gacgccagag 720
ttccaccccc acaagaccac actggcctgg ctccgggaca cataccagc cctgccaccg 780
tctgcacggc ccctggagtg taccatccgg gctgggtgagg tgctgtactt ccccgaccgc 840
tggtggcatg ctacgtctca ccttgacacc agcgtcttca tctccacctt cctcggctag 900
ccaaaacagc tggcaggact gccggtcaca caccagcacg tcc                                     943

```

&lt;210&gt; 287

&lt;211&gt; 1143

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 287

```

gaattcggca cgagggaaga acagctgttg gaacaacaag aatatttaga aaaagaaatg 60
gaggaagcaa agaaaatgat atcaggacta caggccttac tgctcaatgg atccttacct 120
gaagatgaac aggagaggcc cttggccctc tgtgaaccag gtgtcaatcc cgaggaaaca 180
ctgattataa tccaaagtcg tctggatcag agtatggagg agaatcagga cttaaagaag 240
gaactgctga aatgtaaaca agaagccaga aacttacagg ggataaagga tgccttgtag 300
cagagattga ctacgcagga cacatctgtt cttcagctca aacaagagct actgagggca 360
aatatggaca aagatgagct gcacaaccag aatgtggatc tgcagaggaa gctagatgag 420
aggaaccggc tcttggggaga atataaaaaa gagctggggc agaaggatcg ccttcttcag 480
cagcaccagg ccaagttaga agaagcactc cggaactct ctgatgtcag ttaccaccag 540
gtggatctag agcgagagct agaacacaaa gatgtcctct tggetcactg tatgaaaaga 600
gaggcagatg aggcgaccaa ctacaacagt cacaactctc aaagcaatgg ttttctcctt 660
ccaacggcag gaaaaggagc tacttcagtc agcaacagag ggaccagcga cctgcagctt 720
gttcgagatg ctctccgcag cctgcgcaac agcttcagtg gccacgatcc tcagcaccac 780
actattgaca gcttggagca gggcatttct agcctcatgg agcgctgca tggtatggag 840
acgcagaaga aacaagaaag aaagggttcgg gtcaagtcac ccagaactca agtaggtagt 900
gaataccggg agtcctggcc ccctaactca aagttgcctc actcacagag ctctccaact 960

```

gtcagcagca cctgtactaa agtgctctat ttcactgacc ggtcacttac gcccttcatg 1020  
 gtcaatatac caaagagggt ggaggagggt acgttaaagg atttttaaagc agctattgat 1080  
 cggaaggaa atcaccggta tcacttcaaa gcactggatc ctgagtttgg cactgtcaaa 1140  
 gag 1143

<210> 288

<211> 881

<212> DNA

<213> Homo sapiens

<400> 288

gtgagagcgg gccgaggaga ttggcgacgg tgcgcgccgt gttttcgttg gcgggtgcct 60  
 gggctggtgg gaacagccgc ccgaaggaa caccatgatt tcggccgcgc agttgttgga 120  
 tgagttaatg ggccgggacc gaaacctagc cccggacgag aagcgcagca acgtgcgggtg 180  
 ggaccacgag agcgtttgta aatattatct ctgtgggttt tgcctgcgg aattgttcac 240  
 aaatacacgt tctgatcttg gtccgtgtga aaaaattcat gatgaaaac tacgaaaaca 300  
 gtatgagaag agctctcgtt tcatgaaagt tggctatgag agagattttt tgcgatactt 360  
 acagagctta cttgcagaag tagaacgtag gatcagacga ggccatgctc gtttggcatt 420  
 atctcaaaac cagcagtctt ctggggccgc tggcccaaca ggcaaaaatg aagaaaaaat 480  
 tcaggttcta acagacaaaa ttgatgtact tctgcaacag attgaagaat taggggtctga 540  
 aggaaaagta gaagaagccc aggggatgat gaaattagtt gagcaattaa aagaagagag 600  
 agaactgcta aggtccacaa cgtcgacaat tgaaagcttt gctgcacaag aaaaacaaat 660  
 ggaagtgtgt gaagtattgt gagccttttt aatagtagga gatgccagc cccgggtaga 720  
 tgaccatttg atgggaaaac aacacatggg ctatgccaaa attaaagcta ctgtagaaga 780  
 attaaaagaa aagttaagga aaagaaccga agaacctgat cgtgatgagc gtctaaaaaa 840  
 ggagaagcaa gaaagagaaa aaaaaaaaaa aaaaactcga g 881

<210> 289

<211> 987

<212> DNA

<213> Homo sapiens

<400> 289

gaattcggca cgagggactg tggtttccag gaatggtggc gtctcacgct tcttgtgctt 60  
 tttccttttg ggctccgag cggctggggg tgggggactg ggcaggaggc tccctgtaaa 120  
 catttggaact tgggctgggg caggggctgg tgttgggcaa agctgggggt ccaggctgga 180  
 gaagcagggg cccctccaga cgcagccttg ggagactcag catgtgcccc cctccccctca 240  
 tcacagaaca agacaatggt taaaaaccag aacagatgcc cagaaggggg taccatggcc 300  
 attaccagca tctcagacaa gggcaggctt caaacaggga ggcctgtggc aaccctccc 360  
 ctacgtctgg agctgagggg acagggggag ctgagaacaa agagaggaaa gaggagaaaa 420  
 gcggcggggg aacaggcggg gagcgtgatc ttcttgcccc catcttcctc aggggttggg 480  
 gggtaaaaag tcggcgggtg cccatcccg caggccccgc tgccccctcag aagaggccgc 540  
 agtccttcag gttgttcttg atgatgacat cgggtgacggc gtcaaacacg aactgcacgt 600  
 tcttgggtgtc ggtggcgcac gtgaagtgcg tgtagatctc cttggtgtct ttgcgcttat 660  
 tcaggctctc aaacttactc tggatgtagc tggctgcctc atcatatttg ttggccccctg 720  
 tatactcagg gaagcagatg gtcaggggac tgtgtgtgat cttctcctca aacaggctcct 780  
 tcttgttgag gaagaggatg atggacgtgt ctgtgaacca cttgttggtg cagatgctat 840  
 cgaatagctt catgctctca tgcattcggt tcatctctc gtccctcagct agcaccaagt 900  
 cataggcgct caaggctacg cagaagatga tggctgtgac gccctcaaag cagtggatcc 960  
 acttcttccg ctacagaccgc tgaccac 987

<210> 290

<211> 300

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(300)

<223> n = A,T,C or G

<400> 290

gattcaagat	gtacccatt	gactttgaga	aggatgatga	cagcaacttt	catatggatt	60
tcacgtggc	tgcattcaac	ctccgggcag	aaaactatga	cattccttct	gcagaccggc	120
acaagagcaa	gctgattgca	gggaagatca	tcccagccat	tgccacgacc	acagcagccg	180
tggttggcct	tgtgtgtctg	gagctgtaca	aggttgtgca	ggggcaccga	cancttgact	240
cctacangaa	tgggtgcctc	aacttgagcc	ctgcctttct	ttggtttctc	tgaaccctt	300

<210> 291

<211> 352

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(352)

<223> n = A,T,C or G

<400> 291

aaccaagctg	ccaccggggg	tggatcggat	gcggcttgag	aggcatctgt	ctgccgagga	60
cttctcaagg	gtatttgcca	tgccccctga	agagtttgcc	aagctggctc	tgtggaagcg	120
gaatgagctc	aagaagaagg	cctctctctt	ctgatggccc	ccacctgctc	cgggacggcc	180
cccttaccce	tgtctgttca	gggtttttcc	ccggcggggt	gggaggggca	ggaggtgggg	240
tggaaatngg	gtgggcncct	ttcctcaggt	agagnggggg	gccaaaacct	ctgcngtccc	300
cggagnagac	tatggacttt	cttccccctc	acaaggntgg	gggcctcctg	ct	352

<210> 292

<211> 511

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(511)

<223> n = A,T,C or G

<400> 292

cgcgggtggct	gcgcactcng	cctgagaaac	tccgcaagcg	cgcagtgtcg	actccccggt	60
ctatgccagg	cgcattctcag	ctaattccaaa	agtaaattgag	aaacttagaa	aaagattgcc	120
aattccaaat	caacatattt	agagaaaatt	ggaaaaggag	aagcttacta	cagctttatt	180
tgaggacttt	ttaaagaacg	ctgggttcta	tctgtgagct	gcaaattctg	gagcaaaaac	240
cagagacatt	gccagagcaa	acaagaacag	aaatacaaat	ggagaactgg	tcaaaagaca	300
taaccacacag	ttatcttgaa	caagaaacta	cggggataaa	taaaagtacg	canccagatg	360
agcaactgac	tatgaattct	gagaaaagta	tgcattcggaa	atccactgaa	ttagnntaatg	420
aaataacatg	ngagaacaca	gaatggccag	gggcagagat	caacgaattt	tcanatcatc	480
agttcttata	cagatgatga	gtctgtttac	t			511

<210> 293

<211> 526

<212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(526)  
 <223> n = A,T,C or G

<400> 293

gataaaaaga	actttaatgg	aaggcactgt	tgtccaaaat	cacataaagg	gtaagagccc	60
acacgggtacc	accctgctct	cctacttctc	aaacccacat	ccaccaccca	gacaggaggg	120
tgcanacccc	acaggaaatt	acctcccggg	gcactgactg	atatttttcc	ttaaaacaaa	180
aaaatggctg	tctcagacta	ataacagaac	atcttaagag	ctataccagc	tattacagcc	240
tggtaatana	agcagctttc	taanaattcc	caagtttata	anaggcccaa	naaatgcatt	300
tattctgttg	tctattaagc	ctccatgaca	aggagaaagt	tatgagtaaa	tccttggttc	360
atcaggagtt	aagagctgtg	ngcctcatga	ggagttaana	gctgtgtgca	taagcagggt	420
caagaaacaa	actcctgttt	gtttgcctct	ttgatgggtc	aaaaacattc	agctgctttc	480
acctctanga	caaaatgctt	aaagaattta	ctctcatcac	cttggg		526

<210> 294  
 <211> 601  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(601)  
 <223> n = A,T,C or G

<400> 294

actttaaaag	ccaaatatat	ttttaaaaga	tcatgcttat	aataagtaaa	ttacncatta	60
aggaaacatc	aaaataaagt	agatgaataa	aaaggcacac	tcgaaaaatt	tgagcgcaga	120
aaggacagtt	ctttttgttt	tgtttcta	gtcgggaaga	aaagaaagag	atatattaaa	180
atcattgttt	tcaagtgaag	gtttctgtca	ggtgaagtag	ttagcaatgg	cttcttttct	240
cccgtgtcca	aagcaggctc	ttcctgcgct	gacttctgag	gaggngttca	gtcctctgcc	300
atgtataggc	gatacatcaa	ggcgacggcc	actgcagaga	tggcagggat	cacccagttg	360
gtccaccaac	tggaactaga	atcaatagta	gtgataagag	tttccggagg	cttgtttaac	420
tttgggtctg	catctggatg	gagctcccca	atgatgaatg	ttttggacat	ttccctggca	480
tctgtagant	gcccgcacat	ctcaaagtcc	tcagtagcng	tcacctccac	ttgttccctt	540
aaaacttctt	ccccaccagg	atgctcttcc	agaaatttgg	gncaaatacgn	acaccttgtg	600
g						601

<210> 295  
 <211> 262  
 <212> DNA  
 <213> Homo sapien

<400> 295

cccttagccc	caagggccct	gggggcagcc	accctcccgc	ctgtcggccc	gtagatttat	60
caaggggtgtt	atgggcccag	ctttgggggg	ccagtcccga	tgcactttga	ggggtgttgg	120
agaggggact	ccccactcg	cacttaactc	aacggctctc	gggccctggg	gctgttttta	180
ccatgtttgt	ttttgaagct	caggtgtctc	acgtctgggc	tgcaccaggc	gaagagagaa	240
attaaagatt	tgaggttttt	cc				262

<210> 296



<211> 598  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(598)  
 <223> n = A,T,C or G

<400> 296

gtagaaca	ctcagcaaaa	taaaattcct	gtttattggt	ggacaacatt	gtttcacaca	60
tacatcaaac	aggccaaaaa	aaataaacag	caacttcata	gacaaaaaag	gaaaaaaaaa	120
gaaacctttt	atctttggcc	tttttaacca	tctcatacaa	accaactact	tatagtacag	180
ctaagtacat	acacaaaaaa	gttactggaa	tgctcggaat	aagattgttt	ttctgttgct	240
atttttgctt	tttttacaag	gntttttttc	tcctttgaga	ttataatgaa	catggncaca	300
ccacaagtaa	agtcagaagt	aggacagana	acgctccgaa	ggctgggtttg	gtcatccgan	360
atcattaaaa	atggctgacc	ctaacaatat	gtacaaaaat	ataaaatgta	aataaaaaat	420
acaaacaaat	ttccttttta	aagtactttt	aagaaaaaaa	gcagggcctt	ggaagttttg	480
gttctttttt	cctccccctg	tgcaaattct	catggtttgg	gttgggtggn	gganancctg	540
tgatcatctg	gggtggcact	gccccggngg	gcgggagggc	ctctctctcg	aangngac	598

<210> 297  
 <211> 509  
 <212> DNA  
 <213> Homo sapien

<400> 297

agaacacagg	tgctgtgaaa	actaccctta	aaagccaaaa	tgggaaagga	aaagactcat	50
atcaacattg	tcgtcattgg	acacgtagat	tcgggcaagt	ccaccactac	tggccatctg	120
atctataaat	gcggtggcat	cgacaaaaga	accattgaaa	aatttgagaa	ggaggctgct	180
gagatgggaa	agggtctcct	caagtatgcc	tgggtcttgg	ataaactgaa	agctgagcgt	240
gaacgtggta	tcaccattga	tatctccttg	tggaaatttg	agaccagcaa	gtactatgtg	300
actatcattg	atgccccagg	acacagagac	tttatcaaaa	acatgattac	agggacatct	360
caggctgact	gtgctgtcct	gattgtttgct	gctggtgttg	gtgaatttga	agctgggtatc	420
tccaagaatg	ggcaggaccc	gagagcatgc	ccttctgggt	tacacactgg	gtgtgaaaca	480
actaattgtc	ggtgttaaca	aatggatt				509

<210> 298  
 <211> 267  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(267)  
 <223> n = A,T,C or G

<400> 298

gggacggggg	aaaggagacg	cttcttcttc	ttgctgctct	tctcgttccc	gagatcagcg	60
gcggcggtga	ccgcgagtgg	gtcggcaccg	tctccggctc	cggngcncaa	caatgctgac	120
tgatagcgga	ggcggnggca	cctccttnna	ggaggacctg	gactctgtgg	ctccgcgac	180
cgccccagct	ggggcctcgg	agccgcctcc	gccgggaggg	gtcgggtctg	ggatccncac	240
cgngaggctn	tttggggagg	gcggggcc				267

<210> 299

<211> 121  
<212> DNA  
<213> Homo sapien

<400> 299  
ggcacgaggg ccctcggagc tcgtttccag atcgaggtaa gagggacttt cttaaaggcc 60  
tagtctatgg gatggggcgg cggagggaat tttttgagaa ataaaatgaa gctgcagtgt 120  
a 121

<210> 300  
<211> 533  
<212> DNA  
<213> Homo sapien

<400> 300  
aagggtgcaca gtatttgatg caggctgctg gtcttggtcg tatgaagcca aacacacttg 60  
tccttggatt taagaaagat tggttgcaag cagatatgag ggatgtggat atgtatataa 120  
acttatttca tgatgctttt gacatacaat atggagtagt ggttattcgc ctaaaagaag 180  
gtctggatat atctcatctt caaggacaag aagaattatt gtcatcacia gagaaatctc 240  
ctggcaccaa ggatgtggta gtaagtgtgg aatatagtaa aaagtccgat ttagatactt 300  
ccaaaccact cagtgaaaaa ccaattacac acaaagttga ggaagaggat ggcaagactg 360  
caactcaacc actgttgaaa aaagaatcca aaggccctat tgtgccttta aatgtagctg 420  
acaaaagct tcttgaagct agtacacagt ttcagaaaaa acaaggaaaag aatactattg 480  
atgtctggtg gctttttgat gatggaggtt tgaccttatt gataccttac ctt 533

<210> 301  
<211> 560  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1) ... (560)  
<223> n = A, T, C or G

<400> 301  
ataaatgatc cctttttattg taagtaatgc gcaacactgg cctggcctttg cactgcaagc 60  
cctcgggtcaa gatatagtc aataactatg gctgcagggt ccacagttcc acaataacca 120  
tggctgcacg atccacaatt cagacacaga catagagctg ggggtgggtgg aaggggagc 180  
aggggtggcag agtgccggact gtccccagcc ctggcctctc catgcanagt tggcccaggc 240  
agacacaccc catggaatga tgagaaagtg acggcacggc cccttcccac agcaagcctg 300  
gggctgccag gaactgccct tcanaacctt tgggcccagg tcnccctgaa nccccacaac 360  
tttttatctg gaataagtat taaaaaacia taaattaagc aaacaacntg gnccttgaag 420  
gatgttgacc nacatgggtc acagtttttg gcncaaaaaa ataagggtct gtttgctttt 480  
tttggaaggc aggggtttgtg gnttggcctt caaatnattt tcaaaccatt ccccaggag 540  
gganaacccc cgggggggaa 560

<210> 302  
<211> 599  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1) ... (599)

<223> n = A,T,C or G

<400> 302

gcaaagttac	aaattttattg	gtctggaaat	aaatacaaat	atctcattaa	naaactcctc	60
tggaaagact	tgtgcacaat	agtttcccat	ccgtactcag	cctctcttgc	cccgatcccc	120
gacttttcta	ctcaaggcca	gggaaggcct	ccaaggngat	gggcggcagg	taacgagtca	180
ttgccttcta	cgccacctgg	aaggctggac	tacttcctcc	tcccaactgc	ggggteccan	240
aaatcctcgg	gtcccagngg	ctgacttaca	atattcaatt	cactctgacc	aaacttccta	300
tganaaaatc	cacggngagc	caaaatgaaa	agtacaaggc	agtagtacag	gaacctggca	360
gccgcactgg	ccgcccanaa	acgtcagtgg	ngctgccccca	ttcggcgaaa	ggttagggag	420
caggaaaaga	ggaagcagga	gaggggaagga	aagtcccatg	gaatatgtat	tccanaatcc	480
ttacattttc	tcagccaccg	ctccccacgt	gagttcccac	ccccaccccg	acaagaagca	540
aagagttctg	aggatccaag	aacgtgaccg	ggtcanacan	gttcagctac	tgagttcac	599

<210> 303

<211> 591

<212> DNA

<213> Homo sapien

<400> 303

cggagttgta	acgtctccact	gactgataga	gcgaccggcc	gaccatggcg	cccggagtgg	60
cccgcggggc	gacgccgtac	tggaggttgc	gcctcgggtg	cgccgcgctg	ctcctgctgc	120
tcattcccgt	ggccgcgcgc	caggagcctc	ccggagctgc	ttgttctcag	aacacaaaca	180
aaacctgtga	agagtgcctg	aagaacgtct	cctgtctttg	gtgcaacact	aacaaggctt	240
gtctggacta	cccagttaca	agcgtcttgc	caccggcttc	cctttgtaaa	ttgagctctg	300
cacgctgggg	agttttgttg	gtgaactttg	aggcgctgat	catcaccatg	tcggtagtcg	360
ggggaaccct	cctcctgggc	attgccatct	gctgctgctg	ctgctgcagg	aggaagagga	420
gccggaagcc	ggacaggagt	gaggagaagg	ccatgcgtga	gcgggaggag	aggcggatac	480
ggcaggagga	acggagagca	gagatgaaga	caagacatga	tgaaatcaga	aaaaaatatg	540
gcctgtttta	agaagaaaac	ccgtatgcta	gatttgaaaa	caactaaagc	g	591

<210> 304

<211> 441

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(441)

<223> n = A,T,C or G

<400> 304

gctggacgga	gacctgctgg	aggaggagga	gctggaggaa	gcagaggagg	aggaccggtc	60
gtcgctgctg	ctgctgtcgc	cgcccgcggc	caccgcctct	cagacccagc	agatcccagg	120
cgggtccctg	gggtctgtgc	tgctgccagc	cgccaggttc	gatgcccggg	aggcggcggc	180
ggcggcgggg	gtgctgtacg	gaggggacga	tgcccagggc	atgatggcgg	cgatgctgtc	240
ccacgcctac	ggccccggcg	gttgtggggc	ggcggcggcc	gccctgaacg	gggagcaggc	300
ggccctgctc	cggagaaaaga	gcgtcaacac	caccgagtgc	gtcccgggtg	ccagctccga	360
gcacgtcgcc	gagatcgctg	gccgccaggg	ttgtaaaatt	aaagcactga	nagccaagac	420
aaacacgtat	atcaagactc	c				441

<210> 305

<211> 491

<212> DNA

<213> Homo sapien

&lt;400&gt; 305

tgcceatgcc	cccttcttag	cactgcaccg	ccaggtccat	gctgctgcca	ccccagacct	60
gggctttgcc	tgccacctct	gtgggcagag	cttccgaggc	tgggtggccc	tggttctgca	120
tctgcgggcc	cattcagctg	caaagcggcc	catcgcttgt	cccaaatgcg	agagacgctt	180
ctggcgacga	aagcagcttc	gagctcatct	gcggcggtgc	caccctcccg	ccccggaggc	240
ccggcccttc	atatgcggca	actgtggccg	gagctttgcc	cagtgggacc	agctagtgtg	300
ccacaagcgg	gtgcacgtag	ctgaggccct	ggaggaggcc	gcagccaagg	ctctggggcc	360
ccggcccagg	ggccgccccg	cggtgaccgc	cccccgcccc	ggtggagatg	ccgtcgaccg	420
ccccttccag	tgtgcctggt	gtggcaagcg	cttccggcac	aagcccaact	tgatcgctca	480
cccgcgcgtg	c					491

&lt;210&gt; 306

&lt;211&gt; 547

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (547)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 306

tctctttctt	ttaagacagg	aatgtaagcc	acaacattta	caaatacaat	gtttttaactc	60
tctacatgta	ggaagccaac	ctgctccttc	ttgatcttct	tctttggcac	aacctcagtg	120
gattttctctg	attcagaacg	agttctaatt	gatcttctct	gttgccttct	ttctactgay	180
cctgtagaac	cagatgttgc	ttcaggagat	gatacactct	gcgttggcct	ttcattttctc	240
tggttttggtg	tagaaattat	aagcctgtct	tgccccctga	cacttatctc	tgttttgtta	300
ccaattccct	ttgttgaata	aacaaattga	tcgataaatt	tcccatcccc	tgtagcatte	360
tgaagagcaa	acacttggtc	aattttcaca	actggagaca	tgttacactt	ctgcaaatec	420
aggctccctt	tgtgcacccg	taatggaagc	tggttaaggat	ttccttgctg	ccgcagtttt	480
ccaggctatt	ttaacaggcg	gnggctcttc	ctctttccgc	acttgtgtgc	cgcctctggc	540
tatgtct						547

&lt;210&gt; 307

&lt;211&gt; 571

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (571)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 307

cgctgcatgt	gataatgtca	tcattttattt	ttaaatgggt	ctaaattgca	nattttaagtt	60
gattttcaa	caaccctatt	tttaaattac	ttttaatagg	aanaaatgaa	gcaaggacat	120
acataatcta	ctatatattga	aggactcaaa	caaatacatg	tttggctgtg	aattctgtac	180
tctcaccaaa	acagagataa	aaatccacct	aaaatacact	ttccttcatt	tagtgcttgt	240
ggganaaggt	caagtattgc	actttaaaat	tactttcate	taacatttgc	cccaactttc	300
cccctgaatt	cactatatgt	tttcagcaaa	catgatttta	taaattttta	gtataaaaagc	360
aactaggttt	tctaattcaa	ctttggaagg	tttactttac	tctacanagc	tattttttgta	420
aaacggcata	tttacttaca	aaattganag	ataggggcat	ccagctgagg	tacatttcct	480
cccttggcgt	tgagtttctg	gacttgggtc	gggggcacag	gcttgtgtga	ctgccccgtg	540
gcccgatata	tggcctggac	cccaggatgc	g			571

<210> 308  
 <211> 591  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(591)  
 <223> n = A,T,C or G

<400> 308

ctccttatgt	gtctgectac	ttcattcttc	ggcatttcct	gcttatccaa	gttcaccatt	60
tcaggtcacc	actggatata	agttgcctgt	atataattat	caggcatttc	ctgcttatcc	120
aagttcacca	tttcagggtca	ccactggata	tcagttgcct	gtatataatt	atcaggcatt	180
tcttgcttat	ccaagttcac	catttcagggt	caccactgga	tatcagttgc	ctgtatataa	240
ttatcaggca	tttcttgctt	atccaagtcc	accatttcag	gtcaccactg	gatatacagt	300
gcctgtatat	aattatcagg	catttcctgc	ttatccaagt	tcaccatttc	aggtcaccac	360
tggatatcag	ttgcctgtat	ataattatca	ggcatttcct	gcttatccaa	gttcaccatt	420
tcaggtcacc	actggatata	agttgcctgt	atataattat	caggcatttc	ctgcttatcc	480
aaattcagca	gttcagggtca	ccactggata	tcagttccat	gtatacaatt	accagatgcc	540
accgcagtgc	cctgttgggg	gagcaaagga	gaaatntgtg	gaccgaagca	t	591

<210> 309  
 <211> 591  
 <212> DNA  
 <213> Homo sapien

<400> 309

aggggggtgca	cgtactccca	actgtgggtcg	cgtcttcacc	ccttctgctg	ctctcgtggc	60
cccctcgcga	tggcgggcat	cctgttttgag	gatattttcg	atgtgaagga	tattgaccgc	120
gagggcaaga	agtttgaccg	aggtaagtaa	gtgtctcgac	tgcattgtga	gagtgaatct	180
ttcaagatgg	atctaattct	agatgtaaac	attcaaattt	accctgtaga	cttgggtgac	240
aagtttcggt	tggatcatagc	tagtaccttg	tatgaagatg	gtaccctgga	tgatgggtgaa	300
tacaacccca	ctgatgatag	gccttcacag	gctgaccagt	ttgagtatgt	aatgtatgga	360
aaagtgtaca	ggattgaggg	agatgaaact	tctactgaag	cagcaacacg	cctgctgaga	420
ttgagagctg	ctgagtggca	gtgctccaga	atcacgggat	ggggccttct	gtttcagctc	480
tgcgtacgtg	tcctatgggg	gcctgctcat	gaggctgcag	ggggatgcc	acaacctgca	540
tggattcgag	gtggactcca	gagtttatct	cctgatgaag	aagctagcct	t	591

<210> 310  
 <211> 488  
 <212> DNA  
 <213> Homo sapien

<400> 310

tggctctcaag	cctgaagagg	ctccgcccac	aagctggccc	atgaagttag	caatgcctgt	60
ggcttcagtc	aattgtcttg	agactgtgaa	gaggctgaaa	gacaccttc	cgggtggaag	120
aaggagttca	ctgaaaactt	atcttaaact	gaccttccc	tttgagttag	tcttcattcc	180
tctcccatgt	gggaacccag	cctccgatgc	cccggggact	aggggaaaca	gttggaggtc	240
cgtgccgtcc	ccagcctgcc	acgggtgcga	ggacagccaa	gtcctgagtg	actcaagatg	300
cttcacttac	atggaagaaa	cttctaaaac	tctaccgagt	ggtttttgta	tataactaaag	360
ttctatttag	agcttttctg	ttttgggcaa	gttcgctgct	ccttctatct	gggcactttg	420
gtttttgtac	tgtcttttgt	gacggcattg	attgaacatt	ttttactagt	agtcttatga	480
cttttgta						488

<210> 311  
 <211> 511  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(511)  
 <223> n = A,T,C or G

<400> 311

cccgtttntg	nagcaaaaana	gggggaagat	ttataggtag	aggcgacaaa	cctaccgagc	60
ctggtgatag	ctggttgtcc	aagatagaat	cttagttcaa	ctttaaattt	gcccacagaa	120
ccctctaaat	ccccttgtaa	atttaactgt	tagtccaaag	aggaacagct	ctttggacac	180
taggaaaaaa	ccttgtagag	agagtaaaaa	atttaacacc	catagtaggc	ctaaaagcag	240
ccaccaatta	agaaagcgtt	caagctcaac	acccactacc	taaaaaatcc	caaacatata	300
actgaactcc	tcacacccaa	ttggaccaat	ctatcacccct	atagaagaac	taatgttagt	360
ataagtaaca	tgaaaacatt	ctcctccgca	taagcctgcg	tcagattaaa	acactgaact	420
gacaattaac	agcccaatat	ctacaatcaa	ccaacaagtc	attattaccc	tcactgtcaa	480
cccaacacag	gcattgctcat	aaggaaaggt	t			511

<210> 312  
 <211> 591  
 <212> DNA  
 <213> Homo sapien

<400> 312

gaacttgctg	tgaaggaagc	agaaactgat	gaaataaaaa	ttttgctgga	agaaagcaga	60
gcccagcaga	aggagacctt	gaaatctctt	cttgaacaag	agacagaaaa	tttgagaaca	120
gaaattagta	aactcaacca	aaagattcag	gataataatg	aaaattatca	ggtgggctta	180
gcagagctaa	gaactttaat	gacaattgaa	aaagatcagt	gtatttccga	gttaattagt	240
agacatgaag	aagaatctaa	tataacttaa	gctgaattaa	acaaagtaac	atctttgcat	300
aaccaagcat	ttgaaataga	aaaaaaccta	aaagaacaaa	taattgaact	gcagagtaaa	360
ttggattcag	aattgagtgc	tcttgaaaga	caaaaagatg	aaaaaattac	ccaacaagaa	420
gagaaatacg	aagctattat	ccagaacctt	gagaaagaca	gacaaaaatt	ggtcagcagc	480
caggagcaag	acagagaaca	gttaattcag	aagcttaatt	gtgaaaaaga	tgaagctatt	540
cagactgccc	taaaagaatt	taaattggag	agagaagttg	ttgagaaaga	g	591

<210> 313  
 <211> 373  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(373)  
 <223> n = A,T,C or G

<400> 313

ttgattttta	ttctgnattt	tattactgaa	atangttgtc	ctantnatcc	caccccacaa	60
taaaaatntn	acccangccc	cccntttctt	tncctnatnc	cctnttccac	cacaccatcc	120
cggaacaagt	gctccaggat	tccctgcccc	ctggccattt	tggagtgtgn	ccattgggta	180
gcaatgtgga	aaccaccaag	gcctttgtgg	anaaaatgga	gggggttgag	ggagncccan	240
gaggggctna	tttgagggcc	tttgccactt	gctcataggc	gagctcnatc	tcctcntnat	300



ctgnacangt ggaagcaaat tcttcccggg cgtnggnant gctnaagnac cgatgcactc 360  
cccggaaggn ctn 373

<210> 314

<211> 591

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(591)

<223> n = A,T,C or G

<400> 314

cccgtgccgc	cgccgcctcc	tgggaagaga	ggaagcggga	gaggagccca	cgtcgcctgt	60
caccaatat	ctccagecgc	gcagtcccga	agagtgtgaa	atgttcgcct	gcgccaagct	120
cgctgcacc	ccctctctga	tccgagctgg	atccagagtt	gcatacagac	caatttctgc	180
atcagtgtta	tctcgaccag	aggctagtag	gactggagag	ggctctacgg	tatttaattg	240
ggcccagaat	ggtgtgtctc	agctaatacca	aaggagagtt	cagaccagtg	caatcagcag	300
agacattgat	actgctgccca	aattttattgg	tgcaggtgct	gcaacagtag	gagtggctgg	360
ttctggtgct	ggtattggaa	cagtcctttgg	cagccttata	attgggttatg	ccagaaaccc	420
ttcgctgaag	cagcagctgt	tctcatatgc	tatcctggga	tttgccctgt	ctgaagctat	480
gggtctcttt	tgtttgatgg	ttgctttctt	gattttgttt	gccatgtaac	aaattactgc	540
ttgacatggt	ggcattcata	ttaattacng	atgtaattct	gtgtatctta	c	591

<210> 315

<211> 591

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(591)

<223> n = A,T,C or G

<400> 315

aagcccttca	ccaacaaaga	tgctataact	tgtgcaaatt	gcagtgcctt	tgtccacaaa	60
ggctgccgag	aaagtctagc	ctcctgtgca	aaggtcaaaa	tgaagcagcc	caaagggagc	120
cttcaggcac	atgacacatc	atcactgccc	acggtcatta	tgagaaacaa	gccctcacag	180
cccaaggagc	gtcctcggtc	cgcagtcctc	ctggtggatg	aaaccgctac	cacccaata	240
tttgccaata	gacgatccca	gcagagtgtc	tcgctctcca	aaagtgtctc	catacagaac	300
attactggag	ttggcaatga	tgagaacatg	tcaaacacct	ggaaattcct	gtctcattca	360
acagactcac	taaataaaaat	cagcaagggtc	aatgagtcaa	cagaatcact	tactgatgag	420
ggtacagaca	tgaatgaagg	acaactactg	ggagactttg	agattgagtc	caaacagctg	480
gaagcagagt	cttggagtcg	gataatagac	agcaagtttc	taaaacagcc	aaaagaaaga	540
tgtgggtcaa	acngcgagaa	gtaatatatg	agttggatgc	agacagagtt	t	591

<210> 316

<211> 591

<212> DNA

<213> Homo sapien

<400> 316

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gtaaatggaa	aggagattat	gaaaaactgg	agcacaacca	catttacatt	caatggcttt	120

137

tccccctgag	agaacaaggc	ttgaacttct	atgccaaaga	actaactaca	tatgaaattg	180
aggaattcaa	aaaaacaaaa	gaagcaatta	gaagattcct	cctggcttat	aaaatgatgc	240
tagaattttt	tggataaaaa	ctgactgata	aaactggaaa	tggtgctcgg	gctgttaact	300
ggcaggaaag	atttcagcat	ctgaatgagt	cccagcacaa	ctatttaaga	atcactcgtg	360
ttcttaaaaag	ccttggtgag	cttggatatg	aaagttttta	atctcctctt	gtaaaattta	420
ttcttcatga	agctcttgtg	gagaatacta	ttcccaatat	taagcagagt	gctctagagt	480
attttgttta	tacaattaga	gacagaagag	aaaggagaaa	gctcctgcgg	ttcgcccaga	540
aacactacac	gccttcagag	aacttttatct	ggggacccgc	ctcgaaaaga	a	591

&lt;210&gt; 317

&lt;211&gt; 323

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 317

ccaagctacg	gaagcaagtg	gaagagattt	ttaatttgaa	atgtgctcaa	gctcttggac	60
tcaccgaggc	agtaaaagta	ccatatcctg	tgtttgaatc	aaacccggag	ttcttctatg	120
tggagggtt	gccagagggg	attcccttcc	gaagccctac	ctgggttggg	attccacgac	180
ttgaaaggat	cgtccacggg	agtaataaaa	tcaagtctgt	tgtaaaaaaa	cctgaactag	240
ttatttccta	cttgccctcct	gggatggcta	gtaaaataaa	cactaaagct	ttgcagtcct	300
ccaaaagacc	acgaagtcct	ggg				323

&lt;210&gt; 318

&lt;211&gt; 591

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (591)

&lt;223&gt; n = A, T, C or G

&lt;400&gt; 318

gatggcgtag	ttggcttgga	gactggcgcg	gcgttcgtgt	ccgagttctc	tgcagggtcac	60
tagtttcccc	gtagttcagc	tgcacatgaa	tagaacagca	atgagagcca	gtcagaagga	120
ctttgaaaat	tcaatgaatc	aagtgaact	cttgaaaaag	gatccaggaa	acgaagtga	180
gctaaaactc	tacgcgctat	ataagcaggc	cactgaagga	ccttgtaaca	tgcccaaacc	240
aggtgtat	gacttgatca	acaaggccaa	atgggacgca	tggaatgccc	ttggcagcct	300
gcccaggaa	gctgccaggc	agaactatgt	ggatttgggt	tccagtttga	gtccttcatt	360
ggaatcctct	agtcagggtg	agcctggaac	agacaggaaa	tcaactgggt	ttgaaactct	420
ggtggtgacc	tccgaagatg	gcatcacaaa	gatcatgttc	aaccggccca	aaaagaaaaa	480
tgccataaac	actgagatgt	atcatgaaat	tatgcgtgca	cttaaagctg	ccagcaanga	540
tgactcaatc	atcacttggt	ttaacaggaa	atggtgacta	ttacagtagn	g	591

&lt;210&gt; 319

&lt;211&gt; 591

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 319

gaattcggca	cgaggttgct	gctaagcgaa	cgcccttttg	agcttacgga	ggccttctga	60
aagacttcac	tgctactgac	ttgtctgaat	ttgctgccaa	ggctgccttg	tctgctggca	120
aagtctcacc	tgaacacagt	gacagtgtga	ttatgggcaa	tgctcctgcag	agttcttcag	180
atgctatata	tttggcaagg	catgttggtt	tgcgtgtggg	aatcccaaag	gagaccccag	240
ctctcacgat	taataggctc	tgtgggttctg	gttttcagtc	cattgtgaat	ggatgtcagg	300

138

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aaatttgtgt taaagaagct gaagttgttt tatgtggagg aaccgaaagc atgagccaag 360
ctccctactg tgtcagaaat gtgcgttttg gaaccaagct tggatcagat atcaagctgg 420
aagattcttt atgggtatca ttaacagatc agcatgtcca gctcccatg gcaatgactg 480
cagagaatct tgctgtaaaa cacaaaataa gcagagaaga atgtgacaaa tatgccctgc 540
agtcacagca gagatggaaa gctgctaata atgctggcta ctttaatgat g 591

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&lt;210&gt; 320

&lt;211&gt; 591

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (591)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 320

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ggctccggcg tctgcagggg tgcgcgagct aaccctgtggc taggcgagtg gggcggggcg 60
gccggcacca tgtcgaggca ggcgaaccgt ggcaccgaga gcaagaaaat gagctctgag 120
ctcttcaccc tgacctatgg tgccctggtc acccagctat gtaaggacta tgaaaatgat 180
gaagatgtga ataaacagct ggacaaaatg ggctttaaca ttggagtccg gctgattgaa 240
gatttcttgg ctcggtcaaa tggtgggagg tgccatgact ttcgggaaac tgcggatgtc 300
attgccaagg tggcgttcaa gatgtacttg ggcacactc caagcattac taattggagc 360
ccagctgggtg atgaattctc cctcattttg gaaaataacc ccttgggtgga ctttgtggaa 420
cttcctgata accactcacc ccttatttat tccaatctct tgtgtggggg gttgcgggga 480
gctttggaga tgggtccagat ggctngngga ggcccaagtt tgtccaggac accctnaaag 540
gagacgggng tgacagaaat ccggatgaga ttcacagggc ggattganga c 591

```

&lt;210&gt; 321

&lt;211&gt; 260

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (260)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 321

```

ctgcttggct ccacacgtgg gccgccgtag gtattccgac cggtaattcc tcctattggt 60
gtgcagcagc cacattgaag gatagagtgg cagcagaggc caaggatcgt gagttgatgg 120
agtttgctgc tgaaaatgaa gggaagtctg ggggaggtct ccacagcgta gctgaggggg 180
tgcggtctaa tccagagcct ggcagggagg gagtaaggga cttagcaggg gcggaggagt 240
tctgcggngg anaggagggg

```

&lt;210&gt; 322

&lt;211&gt; 559

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (559)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 322

ttccacatga	catggagtgt	gaagctggat	gagcacatca	ttccactggg	aagcatggca	60
nttaacagca	tctcaaaact	gactnancct	acccagtctt	ccatgtattc	acttcctaata	120
gcacccactc	tggcanacct	gnaggacnat	acacatgaag	ncantgatga	tcagccagan	180
aancctcact	ttgactctcg	canngtgata	tttgagctgg	attcatgcaa	tggnagtggg	240
aaagtttgcc	ttgtctacaa	aagtgggaaa	ccagnattag	cagaanacac	tgagatctgg	300
ttcctgnaca	nancgttata	ctggcatttt	ctcacanaca	cctttactgc	ctattaccgc	360
ctgctcatca	cccacctggg	cctgccccag	tggcaatatg	ccttcccagc	tatggcatta	420
gcccacaggc	caagcaatgg	ttcagcatgt	ataaacctat	cacctacaac	acaaacctgc	480
tcacagaaga	naccgactcc	tttgtgaata	agctagatcc	canctnagtg	tttaagagca	540
agaacaagat	cgttatccc					559

&lt;210&gt; 323

&lt;211&gt; 492

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(492)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 323

cctgtctccc	agccgtacca	gagagggctc	ggccggcagc	gccgggctgg	ggggcggcgg	60
cgccggcgcc	ggagccgggg	tgggtgcagg	cggcggcggg	ggcagcgggc	cgagcagcgg	120
cggcggggcc	ggggggctgc	aacccagcag	ccgcgctggc	ggcggccggc	cctccagccc	180
cagcccgtcg	gtggtgagcg	agaaggagaa	ggaagagttg	gagcggctgc	agaaagagga	240
ggaggagagg	aagaagaggg	tgcagctgta	tgtgttcgtg	atgcgctgca	tcgcctaccc	300
ctttaatgcc	aagcagccca	ccgacatggc	tcgccggcag	cagaagatca	gcaaacagca	360
gctgcagaca	gtcaaggacc	ggtttcaggc	tttcctcaat	ggggaaaccc	anatcatggc	420
tgacgaagcc	ttcatgaacc	gctgtngcag	agttactatg	aggtgttcct	gaagaccacc	480
cgtgtggccg	ca					492

&lt;210&gt; 324

&lt;211&gt; 474

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(474)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 324

aatttcagca	acatacttct	caatttcttc	aggatttaaa	atcttgaggg	attgatctcg	60
cctcatgaca	gcaagttcaa	tgtttttgcc	acctgactga	accacttcca	ggagtgcctt	120
gateaccagc	ttaatggtca	natcatctgt	ttcaatggct	tcgtcagtat	agttcttctc	180
cagnaactca	cgcactgact	tggcaccgcc	gcctatggca	ttggccttcc	aggcatggta	240
tgtgcccagag	gggtcagtct	gatagagcct	aggagtggca	tcaaagtcga	aaccacagat	300
gagggcagag	atgccaaacg	gcctgcgcgc	attgctctgc	gtataacgct	gcttcanact	360
ggcgatgtag	cgggtgatgt	actccacagt	gaccgggtcc	tccacagtca	gccggtggct	420
ctggcactcc	acccggggcc	tgttgatgac	tatccttgca	tcggcgggtga	ggcc	474

&lt;210&gt; 325

&lt;211&gt; 532

140

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(532)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 325

gaggagacag	gacagagcgt	ctggagagggc	aggaggacac	cgagttcccc	gtggtggcct	60
ccaggtcctg	tgcttgcgga	gccgtccggc	ggctgggata	gagccccgac	aatgggcaac	120
gcgcaggagc	ggccgtcaga	gactatcgac	cgcgagcgga	aacgcctggt	cgagacgctg	180
caggcggact	cgggactgct	gttggacgcg	ctgctggcgc	ggggcggtgct	caccggggcca	240
gagtacgagg	cattggatgc	actgcctgat	gccgagcgca	gggtgcgccg	cctactgctg	300
ctggtgcagg	gcaagggcga	ggccgcctgc	caggagctgc	tacgctgtgc	ccagcgtacc	360
gcgggcgcgc	cggacccccg	ttgggactgg	cagcacgtgg	gtccgggcta	ccgggaccgc	420
agctatgacc	ctccatgccc	aggccactgg	acgccggagg	caccgggctc	ggggaccaca	480
tgccccgggt	tgcccagact	tcagaccctg	acgaggnccg	gggccctgag	gg	532

&lt;210&gt; 326

&lt;211&gt; 322

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(322)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 326

caaaattaac	atttttatta	aatcaagtta	aaaaaaatgt	tcagtgtana	aaagtcaaca	60
agggttttta	caaaaccaa	atataccttt	ttatacaata	tatgtatata	ttagcagcaa	120
actacttctg	anattctctt	tcttttatgt	tcttctagtt	attttaaaga	aagcataaac	180
aatgtatatt	agtatggaat	gtcagcaaat	ccactcttag	tcctttattc	tgtgatttgg	240
gccttctaca	aaatactttg	tgattctcac	taatgaatat	taagaacata	cccaatttta	300
actaaaaagt	agtgaaacag	tg				322

&lt;210&gt; 327

&lt;211&gt; 387

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 327

aaaaccgtgt	actattagcc	atgggtcaacc	ccaccgtggt	cttcgacatt	gccgtcgacg	60
gcgagccctt	gggccgcgtc	tcctttgagc	tgtttgacga	caaggtccca	aagacagcag	120
aaaattttcg	tgctctgagc	actggagaga	aaggatttgg	ttataagggt	tcctgctttc	180
acagaattat	tccagggttt	atgtgtcagg	gtggtgactt	cacacgccat	aatggcactg	240
gtggcaagtc	catctatggg	gagaaatttg	aagatgagaa	cttcatecta	aagcatacgg	300
gtcctggcat	cttgtccatg	gcaaatgctg	gacccaacac	aaatggttcc	cagtttttca	360
tctgcactgc	caagactgag	tggttgg				387

&lt;210&gt; 328

&lt;211&gt; 502

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(502)  
 <223> n = A,T,C or G

<400> 328

agcagcccgg	cgcggccgcc	gcgcccggcg	gcggcaaggc	tccggggccag	catggggggct	60
tcgtgggtgac	tgtcaagcaa	gagcgcgggcg	aggggtccacg	cgcgggcgag	aaggggtccc	120
acgaggagga	gccggtgaag	aaacgcggct	ggcccaaggg	caagaagcgg	aagaagattc	180
tgccgaatgg	gcccaaggca	ccggtcacgg	gctacgtgcg	cttcctgaac	gagcggcgcg	240
agcagatccg	cacgcgccac	ccggatctgc	cctttcccga	gatcaccaag	atgctggggcg	300
ccgagtggag	caagctgcag	ccaacggaaa	agcagcggta	cctggatgag	gccnagagag	360
agaagcagca	gtacatgaag	gagctgcggg	cgtaccagca	gtctgaagcc	tataagatgt	420
gcacggagaa	gatccaggag	aagaagatca	agaaagaaga	ctcgagctct	gggctcatga	480
acactcttct	gaatggacac	aa				502

<210> 329  
 <211> 463  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(463)  
 <223> n = A,T,C or G

<400> 329

caagttgcac	attttaattt	acaattttta	ccaataaaaa	ggattagttt	acaaaaaggg	60
aagtccttta	tacaaaataa	ggacaatttg	taaaganaat	ccactgtcat	gttttgcctt	120
gtcaagtcaa	aactcaaata	gcttgttttg	gtaaaattat	tccagaaaca	taatccagac	180
aaaatcaata	acgtcatcag	cttcctaacc	atgtttaana	ggaataactt	catgaacatt	240
ttgccctgaa	ctgaanagtt	ctaaataactt	gtaaaccttt	aggaaaaaat	gactgctcgc	300
aggcagcttg	actggtaaga	gggtacacca	nagactccgg	gtcactcact	gtcagaatat	360
tcttatacat	acaatgagtc	tccacgcctg	tacaatgagt	gtcgtgcaac	ataattggag	420
taatggcctc	taaaatttta	caagtaaact	ttattgnggc	ccc		463

<210> 330  
 <211> 500  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(500)  
 <223> n = A,T,C or G

<400> 330

taattataga	tctacaaaat	atgaaatgta	ttccaagaat	gcagaaaaac	catctagaag	60
caaaaggact	ataaaaacaaa	aacagagaag	aaaattcatg	gctaaaccag	ctgaagaaca	120
gcttgatgtg	ggacagtcta	aagatgaaaa	catacataca	tcacatatta	ccaagacga	180
atttcaaaga	aattcagaca	gaaatatgga	agagcatgaa	gagatgggaa	atgatttgtt	240
ttccaaaaaa	acagatgcca	cctgtgggaa	gcaagaaaag	tagcactaga	aaagataagg	300
aagaatctaa	aaagaagcgc	ttttccagtg	agtccaagaa	caaacttgtn	cctgaagaag	360
tgacttcaac	tgtcacgaaa	agtcgaanaa	tttccangcg	tccatctgat	tgggtgggtgg	420



taaaancaga ggagagtcct gtttatagca attcttcagt aagaaatgaa ttaccaantg 480  
catcacaatn ntgcccggaa 500

<210> 331  
<211> 494  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(494)  
<223> n = A,T,C or G

<400> 331  
tctctctctc tctcaaaatt acagtgttca ttgtcattga cctcagcagc aaatttgact 60  
tgaattcact taggatcgca ggaatcaggg gaaagtgatt ttaaagggtgg tttctccagc 120  
acattttaag aaaagggacc aaaagttatt ttagcttcct caatagattg catgttgctt 180  
attaggataa taaattaata ttaaattgcaa tatatgtctt gncctttatta tggcatctat 240  
ttaggagttg ttcaaatacac tgcagttaggg ctctgcaaat aaaataatgn aacctattat 300  
catggatcta atgnactgna actttatcag tgaaaggnaa aatctcaaat aacaagtaca 360  
aacattggac aattacctat aaagatttgt aaaaggaaaa tttttccata gatttcattc 420  
ttggcatttt gttaaagacga ccttgcagnc cctgttttgn aactttttta ataaaataga 480  
catctgttta cttg 494

<210> 332  
<211> 538  
<212> DNA  
<213> Homo sapien

<400> 332  
aaagaacaaa tggaacgcga tgggtgttct gaacaagagt ctcaaccgtg tgcattttatt 60  
gggataggaa atagtgacca agaaatgcag cagctaaact tggaaggaaa gaactattgc 120  
acagccaaaa cattgtatat atctgactca gacaagcgaa agcacttcat gttgtctgta 180  
aagatgttct atggcaacag tgatgacatt ggtgtgttcc tcagcaagcg gataaaagtc 240  
atctccaaac cttccaaaaa gaagcagtca ttgaaaaatg ctgacttatg cattgcctca 300  
ggaacaaagg tggctctgtt taatcgacta cgatcccaga cagttagtac cagatacttg 360  
catgtagaag gaggttaattt tcatgccagt tcacagcagt ggggagcctt ttttattcat 420  
ctcttggatg atgatgaatc agaaggagaa gaattcacag tccgagatgg ctacatccat 480  
tatggacaaa cagtcaaact tgtgtgctca gttactggca tggcactccc aagattga 538

<210> 333  
<211> 499  
<212> DNA  
<213> Homo sapien

<400> 333  
ctcagcctgc gggactgctc ggctcgggctt ctaggcgggtt ttgatgaaca cctggcttta 60  
ttcttgcaat gaagaaagggt tctcaacaaa aaatattctc caaagcaaag ataccatcat 120  
catctcactc tctatccca tcatctatgt ccaatatgag atctaggtca ctttcacctt 180  
tgattggatc agagactcta ccttttctatt ctggaggaca gtggtgtgag caagttgaga 240  
ttgcagatga aaacaatatg ctttttgact atcaagacca taaaggagct gattcacatg 300  
caggagttag atatattaca gaggccctca ttaaaaaact tactaaacag gataatttgg 360  
ctttgataaa atctctgaac ctttcacttt cttaaagacgg tggcaagaaa ttttaagtata 420  
ttgagaattt ggaaaaatgt gttaaacttg aagtactgaa tctcagctat aatctaatag 480  
ggaagattga aaagtcgga 499

<210> 334  
 <211> 561  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(561)  
 <223> n = A,T,C or G

<400> 334

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gaaaattcaa	tgaatcaagt	gaaactcttg	aaaaaggatc	caggaaacga	agtgaagcta	120
aaactctacg	cgctatataa	gcaggccact	gaaggacctt	gtaacatgcc	caaaccaggt	180
gtattttgact	tgatcaacaa	ggccaaatgg	gacgcatgga	atgcccttgg	cagcctgccc	240
aaggaagctg	ccaggcagaa	ctatgtggat	ttggtgtcca	gtttgagtcc	ttcattggaa	300
tcctctagtc	aggtggagcc	tggaacagac	aggaaatcaa	ctgggtttga	aactctggtg	360
gtgacctccg	aagatggcat	cacaaagatc	atgttcaacc	cggcccaaaa	agaaaaatgc	420
cataaacact	gagatgtatc	atgaaattat	gcgtgcactt	aaagctgcca	gcaaggatga	480
ctcaatcatc	actgttttaa	cangaaatgg	tgactattac	agtagtgagg	atgatctgac	540
taacttcnct	gatattcccc	c				561

<210> 335  
 <211> 551  
 <212> DNA  
 <213> Homo sapien

<400> 335

aagctgggtca	tggctgggga	gaccaccaac	tccccgcggcc	agcggctgcc	ccagaaggga	60
gacgtggaga	tgctgtgcgg	cgggcccgcc	tgccagggct	tcagcggcat	gaaccgcttc	120
aattcgcgca	cctactccaa	gttcaaaaac	tctctggtgg	tttccttctc	cagctactgc	180
gactactacc	ggccccgggt	cttcctcctg	gagaatgtca	ggaactttgt	ctccttcaag	240
cgtcccatgg	tcctgaagct	caccctccgc	tgccctggct	gcatgggcta	tcagtgcacc	300
ttcggcgtgc	tgcaggccgg	tcagtacggc	gtggcccaga	ctaggaggcg	ggccatcatc	360
ctggccgcgg	cccctggaga	gaagctccct	ctgttcccgg	agccactgca	cgtgtttgct	420
ccccgggcct	gccagctgag	cgtggtgggt	ggatgacaag	aagtttgtga	gcaacataac	480
caggttgagc	tcgggtcctt	tccggaccat	acggtgcgag	aaacgatgtc	cgacctgccg	540
gaagtgcgga	a					551

<210> 336  
 <211> 540  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(540)  
 <223> n = A,T,C or G

<400> 336

aggtctatgt	ctactgaagg	caataaacga	ggaatgatcc	agcttattgt	tgcaaggaga	60
ataagcaagt	gcaatgagct	gaagtcacct	gggagccccc	ctggacctga	gctgcccatt	120
gaaacagcgt	tggatgatag	agaacgaaga	atttcccatt	ccctctacag	tgggattgag	180
gggcttgatg	aatcgcccag	cagaaatgct	gccctcagta	ggataatggg	taaataaccag	240

144

ctgtccccta	cagtgaatat	gcccccaagat	gacactgtca	ttatagaaga	tgacagggttg	300
ccagtgtctc	ctccacatct	ctctgaccag	tcctcttcca	gctcccatga	tgatgtgggg	360
tttgtgacgg	cagatgctgg	tacttggggc	aaggctgcaa	tcagtgattc	agccgactgc	420
tctttgagtc	cagatgttga	tccagttctt	gcttttcaac	gaaaaaggat	ttggacgtca	480
gaagtatgtc	agaaaaacgc	accaaagcaa	ttttcanatg	ccagtcaatt	ggatttcggt	540

&lt;210&gt; 337

&lt;211&gt; 422

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(422)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 337

gcagcaggaa	cagttacagc	agcagcagca	acagcagctg	ttgcaacagc	agcaggaaca	60
attgcagcag	caacaactgc	agcctcctcc	cctggagccc	gaggaggagg	aagaggtgga	120
gctggagctc	atgccggtgg	acctgggggtc	agagcaggag	ctggagcagc	agcggcagga	180
gttggagcgg	cagcaggagc	tggaaacggca	gcaggagcag	cggcagctgc	agctcaaact	240
gcaggaggag	ctgcagcagc	tggagcaaca	gctggagcag	cagcagcagc	agctggagca	300
gcaggaggtg	cagctggagc	tgaccccggg	ggagctaggg	gcccagcagc	aggaggtgca	360
gctggagctg	acccccgtgc	agccggagct	gcagctggaa	ctggtgccan	cccagggggc	420
gg						422

&lt;210&gt; 338

&lt;211&gt; 601

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(601)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 338

catcttacga	acgctctatg	atgtcttatg	agcgggtctat	gatgtcccct	atggctgaac	60
gctctatgat	gtcagcctac	gagcgctcta	tgatgtcagc	ctacgagcgc	tctatgatgt	120
cccctatggc	tgagcgctct	atgatgtcag	cttatgaacg	ctccatgatg	tcagcttatg	180
aacgctccat	gatgtcccca	atggctgate	gatctatgat	gtccatgggt	gctgaccggg	240
ctatgatgtc	gtcatactct	gctgctgacc	ggctctatgat	gtcatcgtag	tctgcagctg	300
accgatctat	gatgtcatct	tatactgctg	atcgttcaat	gatgtctatg	gctgctgatt	360
cttacaccga	ttcttacact	gacacatata	cagaggcata	tatgggtgcca	cctttgcctc	420
ctgaagagcc	cccaacaatg	ccaccgttgc	cacctgagga	gccaccaatg	acaccaccat	480
tgctnctga	ggaaccaccc	agaggggtcca	gcattgceca	cttgagcagt	cagcattaac	540
cagcttgaaa	atacttggcc	ctacanangg	tgccatcatt	accatctgaa	gagctgtatc	600
g						601

&lt;210&gt; 339

&lt;211&gt; 440

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

<221> misc\_feature  
<222> (1)...(440)  
<223> n = A,T,C or G

<400> 339  
agagggagga ggcccaactg gtgatgctgc tgctgctgct gctgccgccg ccgccgcctc 60  
tattgctgat actctagtgg ggctggaagg gtggttccta ttcgcaccat cgccaaccag 120  
agacagaggg aaaaaaaaaa ccggcagcca ctgctgatgt tgggttcgga ggctgcatcc 180  
gactcgggtca caaggaaaat ggattcagtt tgcattctctc cctcctttaa acagcttctc 240  
cgggtctcag catggtatca aagcttgaaa gagagaagac tcaagaagcg aagaggattc 300  
gtgagctgga gcagcgcaag cacacgggtgc tgggtgacaga actcaaagcc aagctccatg 360  
aggagaagat gaaggagctg caggctgtga gggagaacct tatcaagcag cacgacagga 420  
aatgtcaang acggtgaagg 440

<210> 340  
<211> 450  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(450)  
<223> n = A,T,C or G

<400> 340  
gattttccagg ggcggatatt gagtgtcgcac ccagaggaag aaagggagga gggcccgcct 60  
aggattcctc aggccgacca gtggaagtct tcaaacaaga gcctgggtgga ggctctgggg 120  
ctggaagccg aggggtgcagt tcctgagaca cagactttga ccggatggag taaggggttc 180  
attggcatgc acagggaat gcaagtcaac cccatttcaa agcggatggg gcccatgact 240  
gtggtcagga tggacgcttc agtccagcca ggcctttttc ggaccctgct ccagtttctt 300  
tatacgggac aactggatga aaaggaaaag gattttggtgg gcctgggtca gatcgcagag 360  
gtcctcgaga tgttcgattt gaggatgatg gtggaaaaca tcatgaacaa ggaagccttc 420  
atgaaccagg agattacgaa nncctttcac 450

<210> 341  
<211> 451  
<212> DNA  
<213> Homo sapien

<400> 341  
aacagctatt aaaacagaaa atggatgaac ttcataagaa gttgcatcag gtgggtggaga 60  
catcccatga ggatctgccc gcttcccagg aaaggtccga ggtaatcca gcacgtatgg 120  
ggccaagtgt aggtcccag caggaactga gagcgccatg tcttccagta acctatcagc 180  
agacaccagt gaacatggaa aagaacccaa gagaggcacc tcctgttggt cctcctttgg 240  
caaattgctat ttctgcagct ttgggtgtccc cagccaccag ccagagcatt gctcctcctg 300  
ttccttttgaa agcccagaca gtaacagact ccatgtttgc agtggccagc aaagatgctg 360  
gatgtgtgaa taagagtact catgaattca agccacagag tggagcagag atcaaagaag 420  
gggtgtgaaac acataagggt gccaacacaa g 451

<210> 342  
<211> 498  
<212> DNA  
<213> Homo sapien

<220>

146

<221> misc\_feature  
 <222> (1)...(498)  
 <223> n = A,T,C or G

<400> 342

ctcaagcagg	ctattgaaga	ggaaggaggc	gatccagata	atattgaatt	aactgtttca	60
actgatactc	caaacaagaa	accaactaaa	ggcaaaggta	aaaaacatga	agcagatgag	120
ttgagtggag	atgcttctgt	gggaagatga	tgcttttatc	aaggactgtg	aattggagaa	180
tcaagaggca	catgagcaag	atggaaatga	tgaactaaag	gactctgaag	aatttggtga	240
aaatgaagaa	gaaaatgtgc	attccaagga	gttactctct	gcagaagaaa	acaagagagc	300
tcatgaatta	atagaggcag	aaggaataga	agatatagaa	aaagaggaca	tcgaaagtca	360
ggaaattgaa	gctcaagaag	gtgaagatga	tacctttcta	acagcccaag	atgggtgagga	420
agaagaaaat	gagaaagata	tagcagggtt	ctgggtgatgg	cncacaagaa	gtatntaaac	480
ctcttccttc	aaaaaggg					498

<210> 343  
 <211> 491  
 <212> DNA  
 <213> Homo sapien

<400> 343

ccgaccccta	ctcggcggcg	caactccaca	accagtacgg	ccccatgaat	atgaacatgg	60
gtatgaacat	ggcagcagcc	gcggcccacc	accaccacca	ccaccaccac	caccccggtg	120
cctttttccg	ctatatgcgg	cagcagtgca	tcaagcagga	gctaactctg	aagtggatcg	180
accccgagca	actgagcaat	cccaagaaga	gctgcaacaa	aactttcagc	accatgcacg	240
agctgggtgac	acacgtctcg	gtggagcacg	tcggcggccc	ggagcagagc	aaccacgtct	300
gcttctggga	ggagtgtccg	cgcgagggca	agcccttcaa	ggccaaatac	aaactggtca	360
accacatccg	cgtgcacaca	ggcgagaaac	ccttccttgc	ccttcggggt	gtggcaaagt	420
cttcgcgcgc	tccgagaacc	tcaagatcca	caaaaggacc	acacagggga	gaagccgtcc	480
agtggagttg	a					491

<210> 344  
 <211> 412  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(412)  
 <223> n = A,T,C or G

<400> 344

gtgcgctgtc	ttcccgtttg	cgtcaggggac	ctgcccagact	cagtggccgc	catggcatca	60
gatgaaggca	aactttttgt	tggagggctg	agttttgaca	ccaatgagca	gtcgctggag	120
caggtcttct	caaagtacgg	acagatctct	gaagtgggtg	ttgtgaaaga	cagggagacc	180
cagagatctc	ggggattttg	gtttgtcacc	tttgagaaca	ttgacgacgc	taaggatgcc	240
atgatggcca	tgaatgggaa	gtctgtagat	ggacggcaga	tccgagtaga	ccaggcaggc	300
aagtcgtcan	acaaccgatc	ccgtgggtac	cgtgggtggct	ctgccggggg	ccggggcttc	360
ttccgtgggg	gcccgangac	ggggcccgtg	ggttctctaa	aagaagaggg	ga	412

<210> 345  
 <211> 498  
 <212> DNA  
 <213> Homo sapien

&lt;400&gt; 345

aactagtctc	gggccatcct	ttctgcgcac	ccggtgtcgc	tgggctgcac	cccgggcggg	60
gacgtccgcc	gggcacggga	gggggcccaag	atgccgatca	ataaatcaga	gaagccagaa	120
agctgcgata	atgtgaaggt	tgttgtagg	tgccggcccc	tcaatgagag	agagaaatca	180
atgtgctaca	aacaggctgt	cagtgtggat	gagatgaggg	gaactatcac	tgtacataag	240
actgattctt	ccaatgaacc	tccaaagaca	tttacttttg	atactgtttt	tggaccagag	300
agtaaacaac	ttgatgttta	taacttaact	gcaagaccta	ttattgattc	tgtacttgaa	360
ggctacaatg	ggactatttt	tgcataatga	caaaccggaa	caggcaaaac	ttttaccatg	420
gaaagggtgc	gagctattcc	tgaacttaga	ggaataattc	cccaatttct	ttgctcacia	480
tatttgggcc	atatttgc					498

&lt;210&gt; 346

&lt;211&gt; 427

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (427)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 346

agatggcggt	cgccgtgaga	actttgcagg	aacagctgga	aaaggccaaa	gagagtctta	60
agaacgtgga	tgagaacatt	cgcaagctca	ccgggcggga	tccgaatgac	gtgaggccca	120
tccaagccag	attgctggcc	ctttctgggc	ctggtggagg	tagaggacgt	ggtagtattat	180
tactgaggcg	tggattctca	gatagtggag	gaggaccccc	agccaaacag	agagaccttg	240
aaggggcagt	cagtaggctg	ggcggggagc	gtcggaccag	aagagaatca	cgccaggaaa	300
gcgaccggga	ggatgatgat	gttaaaaagc	cagcattgca	gtcttcannt	gtagctacct	360
cccaaagagc	gccccacgta	gagaccttat	ccagggatca	aaattttgga	tgaaaaaggg	420
gaaagcc						427

&lt;210&gt; 347

&lt;211&gt; 280

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 347

cacagaaagt	tctecgtccc	cagacatggg	tccctcggct	tcctgcctcg	gaagcgcagc	60
agcaggcatc	gtgggaaggt	gaagagcttc	cctaaggatg	accggtccaa	gccgggtccac	120
ctcacagcct	tcctgggata	caaggctggc	atgactcaca	tcgtgcggga	agtcgacagg	180
ccgggatcca	aggtgaacaa	gaaggaggtg	gtggaggctg	tgaccattgt	agagacacca	240
cccatggtgg	ttgtgggcat	tgtgggctac	gtggaaaccc			280

&lt;210&gt; 348

&lt;211&gt; 411

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 348

caactatgat	gtgcctgaaa	aatgggcacg	attctatact	gcagaagtag	ttcttgcatt	60
ggatgcaatc	cattccatgg	gttttattca	cagagatgtg	aagcctgata	acatgctgct	120
ggataaatct	ggacatttga	agtttagcaga	ttttgggtact	tgtatgaaga	tgaataagga	180
aggcatggta	cgatgtgata	cagcgggttg	aacacctgat	tatatattccc	ctgaagtatt	240
aaaatcccaa	ggtggtgatg	gttattatgg	aagagaatgt	gactggtggt	cggttggggg	300
atttttatac	gaaatgcttg	taggtgatac	acctttttat	gcagattctt	tggttggaac	360



ttacagtaaa attatgaacc attaaaaatt cacttacctt tcctgatgat a

411

<210> 349

<211> 408

<212> DNA

<213> Homo sapien

<400> 349

gatgggcatc	tctcgggaca	actggcacaa	gcgcccga	accgggggca	agagaaagcc	60
ctaccacaag	aagcggaagt	atgagttggg	gcgcccagct	gccaacacca	agattggccc	120
ccgcccgcac	cacacagtcc	gtgtgcgggg	aggtaacaag	aaataccgtg	ccctgagggt	180
ggacgtgggg	aattttctct	ggggctcaga	gtgttggtact	cgtaaaacaa	ggatcatcga	240
tggtgtctac	aatgcatcta	ataacgagct	ggttcgtacc	aagaccctgg	tgaagaattg	300
catcgtgctc	atcgacagca	caccgtaccg	acagtgggtac	gagtcceact	atgcgctgcc	360
cctggggccgc	aagaagggag	ccaaactgac	ttctgaggaa	gaagaaaa		408

<210> 350

<211> 409

<212> DNA

<213> Homo sapien

<400> 350

ggttccccca	gctctgggta	cccggctctg	catcgcgtcg	ccatgatggg	ccatcgtcca	60
gtgctcgtgc	tcagccagaa	cacaaagcgt	gaatccggaa	gaaaagttca	atctggaaac	120
atcaatgctg	ccaagactat	tgcagatata	atccgaacat	gtttgggacc	caagtccatg	180
atgaagatgc	ttttggaccc	aatgggaggc	attgtgatga	ccaatgatgg	caatgccatt	240
cttcgagaga	ttcaagtcca	gcatccagcg	gccaagtcca	tgatcgaaat	tagccggacc	300
caggatgaag	aggttggaga	tgggaccaca	tcagtaatta	ttcttgcagg	ggaaatgctg	360
tctgtagctg	agcacttcct	ggagcagcag	atgcacccaa	caggtgggg		409

<210> 351

<211> 226

<212> DNA

<213> Homo sapien

<400> 351

aatcccaaac	atataactga	actcctcaca	cccaattgga	ccaatctatc	accctataga	60
agaactaatg	ttagtataag	taacatgaaa	acattctcct	ccgcataagc	ctgcgtcaga	120
ttaaaacact	gaactgacaa	ttaacagccc	aatatctaca	atcaaccaac	aagtcattat	180
taccctcact	gtcaacceaa	cacaggcatg	ctcataagga	aaggtt		226

<210> 352

<211> 410

<212> DNA

<213> Homo sapien

<400> 352

gcggaggggc	tggtctgggca	ggaggggttg	gcggggcagc	agggccgcgg	ccatggggag	60
cttgaaggag	gagctgctca	aagccatctg	gcacgccttc	accgcactcg	accaggacca	120
cagcggcaag	gtctccaagt	cccagctcaa	ggtcctttcc	cataacctgt	gcacgggtgct	180
gaaggttcct	catgacccag	ttgcccttga	agagcacttc	agggatgatg	atgaggggtcc	240
agtgtccaac	cagggctaca	tgccttattt	aaacagggttc	attttggaaa	aggtccaaga	300
caactttgac	aagattgaat	tcaataggat	gtgttggtgac	ctctgtgtca	aaaaaaacct	360
cacaaagaat	cccctgctca	ttacagaaga	agatgcattt	aaaatatggg		410

<210> 353  
 <211> 380  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(380)  
 <223> n = A,T,C or G

<400> 353  
 gagtttatttt agaaagtatc atagtgtaaa caaacaatt gtaccacttt gattttcttg 60  
 gaatacaaga ctctgatgc aaagctgaag ttgtgtgtac aagactcttg acagttgtgc 120  
 ttctctagga ggntgggttt ttttaaaaaa agaattatct gngaaccata cgtgattaat 180  
 aaagatttcc tttaaggcan aggctggctn agatgctgct gttatcttct gcctcagaca 240  
 gacagtataa gnggtcttgt ttctaagatt cctaccacca gttactttgg gccaaagtatc 300  
 cacatcccct tgcgtatggg aggnnggtga anagtgttgg atgcaaagng gttattatgg 360  
 gaagnagctc natggtaaaa 380

<210> 354  
 <211> 379  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(379)  
 <223> n = A,T,C or G

<400> 354  
 caacacatct ttattaaaca cctgaagtta ctgggaggag gccatgatgc tggacacact 60  
 gtcaaagtca atcttctcca caatgttctt gggtttaatg ctctcttctt ggctacagan 120  
 gaanatctgc cccgactngt cggcactcca gccgtatttg ctcatccaca cctttagctg 180  
 gctgtccgac aganccccga gcatntcggc cagcagccan cggncaatgt gctggtaagt 240  
 gatacccaca acatggcaga taaactttcg gacanagtct tcaaagccag ttataccttc 300  
 caagagggtcc atgttttcat ccagggttg ccanaagcct ggaaatggca ggtctccaac 360  
 aggtccccca ggtacaaaa 379

<210> 355  
 <211> 499  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(499)  
 <223> n = A,T,C or G

<400> 355  
 gtccagagct gctggtgctc ccgttccccca gaccctaccc ctatccccag tggagccgga 60  
 gtgcggggcgc gccccaccac cgcctcacc atggtgctgt tggcagcagc ggtctgcaca 120  
 aaagcaggaa aggctattgt ttctcgacag tttgtggaaa tgaccggaac tcggattgag 180  
 ggcttattag cagcttttcc aaagctcatg aacactggaa aacaacatac gtttgttgaa 240  
 acagagagtg taagatatgt ctaccagcct atggagaaac tgtatatggt actgatcact 300  
 accaaaaaca gcaacatttt agaagatttg gagaccctaa ggctcttctc aagagtgatc 360

150

cctgaatatt gcgagcctta gaagagaatg aaatatctga gcactgnntt gatttgattt 420  
ttgcttttga tgaaaatgtc gcactgggat acccgggang aatgttaact tggcacagat 480  
canaaccttt cacagaaaa 499

<210> 356  
<211> 511  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(511)  
<223> n = A,T,C or G

<400> 356  
gggcttctgc tgaggggggca ggcggagctt gaggaaaccg cagataagtt tttttctctt 60  
tgaaagatag agattaatac aactacttaa aaaatatagt caatagggtta ctaagatatt 120  
gcttagcggtt aagttttttaa cgtaatttta atagcttaag attttaagag aaaatatgaa 180  
gacttagaag agtagcatga ggaaggaaaa gataaaaagg ttctaaaaca tgacggagggt 240  
tgagatgaag cttcttcacg gagtaaaaaa tgtattttaa agaaaattga gagaaaggac 300  
tacagagccc cgaattaata ccaatagaag ggcaatgctt ttagattaaa atgaagggtga 360  
cttaaacagc ttaaagttta ntttaaaagt tgtagggtgat taaaataatt tgaaggcgat 420  
cttttaaaaa gagattaaac ccgaagggtga ttaaagacc ttgaaatcca tgacgccagg 480  
gagaattgcc gtcattttaa gcctagttaa c 511

<210> 357  
<211> 511  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(511)  
<223> n = A,T,C or G

<400> 357  
gatacttcac atttccctag ggacgggagc ccgagggggtc cgttcggccc tcttcctctc 60  
gctgggcccga caccgcgtg taggaccgta acccttagtc ccaatgcctc cgtaagcgga 120  
gttgagtggtg tgccgtgtgtg tggagctgtg gaggtgtccc cgggtggcgag cgcggccaga 180  
actgcggtca cttaagtttt ccgtgtgcgg gttgcaagga gcgtgcgtgc gtctggtata 240  
atttggtctc ctgagattct gcttacaaga aaggagtggg aaataccctt ggaaagaaaa 300  
ctaaaacagt aagaaaacca aaacttattt ttacatggnt gtcagcacat ttaccgatat 360  
ggacactttt cccaataatt tcctcctggt ggagacagtg gattgacagg ttctcagtcg 420  
gaattccaga aaaatgttaa ttgatgaaaa gggtacnatg tgagcatcat aaagntaatt 480  
attaanacac tgaaggctga acacacaagg g 511

<210> 358  
<211> 401  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(401)  
<223> n = A,T,C or G

151

&lt;400&gt; 358

acggatgaag	atgatgacct	tcaagaaaat	gaagacaata	aacaacataa	agaaagcttg	60
aaaagagtga	cctttgcttt	accagatgat	gcggaaactg	aagatacagg	tgttttaaat	120
gtaaagaaaa	attctgatga	agttaaattc	tcctttgaaa	aaagacagga	aaagatgaat	180
gaaaaaattg	catctttaga	aaaagagttg	ttagaaaaaa	agcccgtggc	agcttcaggg	240
ggaagtgaca	gcacagaaga	ggccagagaa	cacctcctgg	aggagaccct	acctttgcca	300
tctgcccgat	ggccctgtga	ttacagagga	acccccctca	ctggagattt	ctttaacnga	360
ngatagagat	cngnttggga	tatgtntcct	taagaaaacc	t		401

&lt;210&gt; 359

&lt;211&gt; 511

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(511)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 359

gcgatgcccg	cgcgcccagg	acgcctcctc	ccgctgctgg	cccggccggc	ggccctgact	60
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gaggcgggcg	cggcggcggc	ggacggggccc	cccgcggcag	acggcgagga	cggacaggac	180
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gcacttcgtc	atgttcttcg	cgccctgggt	tggacacttg	ccagcggttt	gcagccgant	300
ttggaatgac	cttggganga	acaaatacaa	cagcatggaa	agaatgccaa	aagtctatgt	360
ggnttaaaagt	ggacttgcac	nggccacttc	gactngtgct	cccccaaggg	gngggaagat	420
accacacctta	aaacttttca	accaagccaa	aaactttgaa	aaccagggtct	cggattcaaa	480
atggaaaact	gatgttcaac	ctgaacaaga	a			511

&lt;210&gt; 360

&lt;211&gt; 511

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(511)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 360

tactgggaga	ctttgagatt	gagtccaaac	agctggaagc	agagtcttgg	agtcggataa	60
tagacagcaa	gtttctaaaa	cagcaaaaga	aagatgtggt	caaacggcaa	gaagtaatat	120
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cnagccnggg	gatgatggcg	gatctgnttt	ttgagcanca	gatggtagaa	aaagctgggt	240
ccctgttttg	atgagcttga	tcagtatccc	atacccatct	tttccagagg	attcttggag	300
ccggaaagaa	nggagtcttc	ttggtgggat	aaaaagtga	aaagaacttt	ctcttcaana	360
aggatagggg	gatgtgcttt	gtaaaatcan	tttttcaggg	ngganaatgc	cnnaaccgtt	420
ttaaagaaaa	acatnttggg	naagtttttg	tgggccaaca	ttacccgggtc	ttgtaaacct	480
accttcaaag	aacctttttg	cccagggtta	a			511

&lt;210&gt; 361

&lt;211&gt; 411

&lt;212&gt; DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(411)

<223> n = A,T,C or G

<400> 361

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ctcttggtg	tgcacgccgc	ggtgaggccg	ctgggcggcg	ggccagacgc	cgaagcacia	180
cttgccggagg	ctgcagctta	acgcggaccc	tgagaagcct	ggcgcttncn	gctggaactt	240
cttggcgcg	gacctggggc	ggtaatttga	gtggccctga	gtcatttcta	caccatccag	300
gccaccaca	cgactaagct	cacaagaagg	ctgaactnnc	tgattctnaa	cctagaanta	360
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<210> 362

<211> 511

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(511)

<223> n = A,T,C or G

<400> 362

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cctcccgtct	ttggctcggt	ggctgccgcc	gccgggggctt	cgccagcctt	caagtcgaga	180
ctactggccg	aaggggcgtc	tgccgctctc	cgccgtcccc	agccctgcct	ctccctgggc	240
tctgccatgg	caatgacagg	ctcaacacct	tgctcatcca	tgagtaacca	cacaaaggaa	300
agggtgacaa	tgaccaaaaag	tgacactgga	gaatttttat	agcaacctta	tcgctcacat	360
gaagaacgag	aaatgagaca	aaagaagtta	gaaaaagggg	atggaagaag	aaggcctaaa	420
aaaatgaagg	agaaaaccaa	cttccgaaga	tcaaccacat	tgcttcggaa	anggaacaaa	480
aantttcttt	cgtttgaaan	aaaaacaaan	a			511

<210> 363

<211> 401

<212> DNA

<213> Homo sapien

<400> 363

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ccagctcggg	cggccacctg	tctttgcccgc	ggtgaccctt	ctctcatgac	cctgcgggtgc	180
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acaggatggt	actggggaag	tatgactggt	aatgaagcca	aagagaaatt	aaaagaggca	360
ccagaaggaa	ctttcttgat	tagagatagc	tcgcattcag	a		401

<210> 364

<211> 401

<212> DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 364

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gaaaatcagg	aaaaaaattt	tttttcaata	atcttattcc	ctatatataa	ttagatttga	120
agaggattaa	cgttgtttta	gtttgggtcc	agatcagcct	tataacaacat	ttctaaactc	180
atttgtactt	ttaaaaaatt	taaacacaga	cttctaaaat	tacttgatgt	aagtaattta	240
aatcacttat	gaccaagtta	ttaaccttat	gaatcagaag	tctgaccctt	gtaggaaatt	300
atattcacat	ataaagtaca	tcagatcttt	gccatatatt	gatggttatt	atgcataaac	360
acattgagtt	gtgttggaag	cagatttata	aacctgcatg	t		401

&lt;210&gt; 365

&lt;211&gt; 361

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 365

atctggagtt	gcacaaatag	ttcttttagaa	cataaaaacta	aatggattta	tacataacag	60
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tcttactcag	aacgtctgat	gtttcccata	atagacagaa	aaaatgcagt	tgtatgagca	240
actgagtttc	ttttcatctt	caaattcatt	tgtgatgggtg	ggaagatcta	aggacaatcc	300
ttccattgaa	gaagtaggaa	aaacagttca	gcactgttct	gaactcatca	aaaatgaaat	360
t						361

&lt;210&gt; 366

&lt;211&gt; 401

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 366

cgggagcagc	agaggtctag	cagccgggcg	ccgcggggccg	ggggcctgag	gaggccacag	60
gacggggcgtc	ttcccggcta	gtggagcccg	gcgcggggcc	cgctgcggcc	gcaccgtgag	120
gggaggaggc	cgaggaggac	gcagcgccgg	ctgccggcgg	gaggaagcgc	tccaccaggg	180
cccccgacgg	cactcgttta	accacatccg	cgctctgtct	ggaaacgctt	gctggcgctt	240
gtcaccgggt	ccctccattt	tgaaagggaa	aaaggctctc	cccacccatt	cccctgcccc	300
taggagctgg	agccggagga	gccgcgtca	tggcggttcag	cccgtggcag	atcctgtccc	360
ccgtgcagtg	ggcgaaatgg	acgtggtctg	cggtacgcgg	c		401

&lt;210&gt; 367

&lt;211&gt; 401

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 367

catggagtcg	ggcaagatgg	cgcctcccaa	gaacgctccg	agagatgcct	tggatgatggc	60
acagatcctg	aaggatatgg	gaatcacaga	gtatgaacca	agggttataa	atcaaattgtt	120
ggaatttgct	ttccgttatg	tgactacaat	tctggatgat	gcaaaaattt	attcgagcca	180
tgctaagaaa	cctaattgtg	atgcagatga	tgtgagactg	gcaatccagt	gtcgtgctga	240
ccaatctttt	acctctcttc	ccccaaagaga	ttttttactg	gatatcgcaa	ggcagaaaaa	300
tcaaaccctt	ttgccactga	ttaagccata	tgcaggacct	agactgccac	ctgatagata	360
ctgcttaaca	gctccaaact	ataggctgaa	gtccttaatt	a		401

&lt;210&gt; 368

&lt;211&gt; 401



154

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 368

cggagcggta	ggagcagcaa	tttatccgtg	tgcagcccca	aactggaaag	aagatgctaa	60
ttaaagtga	gacgctgacc	ggaaaggaga	ttgagattga	cattgaacct	acagacaagg	120
tggagcgaat	caaggagcgt	gtggaggaga	aagagggaat	ccccccacaa	cagcagaggc	180
tcatctacag	tggcaagcag	atgaatgatg	agaagacagc	agctgattac	aagattttag	240
gtggttcagt	ccttcacctg	gtgttggtc	tgagaggagg	aggtggtctt	aggcagtgat	300
ggaccctcca	ttttacctct	ttaccctgtc	gtccataatg	aggcatcata	tatcctctca	360
ctctctggga	caccatagcc	ctgccccctc	ccctggatgc	c		401

&lt;210&gt; 369

&lt;211&gt; 174

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (174)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 369

gcgagnnggg	cgccaagcgc	ggggccggag	cggccttccc	ggagtccttt	gcgcgggcacc	60
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ccccgcgggc	ggtggcgggtg	gcgggagccg	ttgggctgag	tcgggacg	ggac	174

&lt;210&gt; 370

&lt;211&gt; 375

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (375)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 370

tgcttttcca	actttattta	gaaaaacaaa	tccagggtccc	agtgccccct	gtaccctccc	60
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ttgggggtcac	ggtggaagga	ggaaganagc	ccactacagc	cgccgcagcg	cccgtttctt	180
gtccgtcttt	ttcttggtcg	ccagcttctt	atcgcgctcg	ccagcatgct	tnttggtccat	240
gggaccctca	gcccctccc	ggccccctgg	ggccccaggg	tcggtggagg	aagcttcagt	300
gccactggcc	agggcccgac	cggcttcggc	cctgcccgtg	ggccccgccg	cgcccccggtg	360
gatctctgtg	agcag					375

&lt;210&gt; 371

&lt;211&gt; 375

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (375)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 371

taaattctaa	aaaatatttt	aatacttgaa	aacttctaaa	acaaaaggta	aggtaacatg	60
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aaagcaaaac	ataacattcg	gagaaagaga	ccagtaactg	acctatttat	tttatattat	180
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ttccctggaa	cactcanagt	ctgcactttt	cctgcaaattg	ggaccatgtc	tgattattta	360
ttatgaaaga	acact					375

&lt;210&gt; 372

&lt;211&gt; 164

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (164)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 372

cgctctgtnt	cctcaacctc	tacctggcgg	aggttatatg	taaagtcaga	tgtgccactg	60
aacttgacag	acacaaaatt	ctactgcatt	tgggctttat	aatggcaagc	ctgctctttt	120
tagtggtgaa	cttgacttgc	gcaatgctag	ttcatggaga	tgtc		164

&lt;210&gt; 373

&lt;211&gt; 401

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 373

gcgctgttcg	cctttgccta	cctgcagctg	tggcggtctgc	tcctgtaccg	cgagcggcgg	60
ctgagttacc	agagcctctg	cctcttctctc	tgtctcctgt	gggcagcgtc	caggaccacc	120
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ctgcacttct	tccccactg	gctgctctac	tgcttccccct	cctgtctcca	gttctccacg	240
ctctgtctcc	tcaacctcta	cctggcggag	gttatatgta	aagtcagatg	tgccactgaa	300
cttgacagac	acaaaattct	actgcatttg	ggctttataa	tggcaagcct	gctcttttta	360
gtggtgaact	tgacttgcgc	aatgctagtt	catggagatg	t		401

&lt;210&gt; 374

&lt;211&gt; 401

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 374

ggaatgatac	cattcagatt	gatttggaga	ctggcaagat	tactgatttc	atcaagttcg	60
acactggtaa	cctgtgtatg	gtgactggag	gtgctaacct	aggaagaatt	ggtgtgatca	120
ccaacagaga	gaggcaccct	ggatcttttg	acgtggttca	cgtgaaagat	gccaatggca	180
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tttctcttcc	ccgaggaaag	ggtatccgcc	tcaccattgc	tgaagagaga	gacaaaagac	300
tggcggccaa	acagagcagt	gggtgaaatg	ggtccctggg	tgacatgtca	gatctttgta	360
cgtaattaaa	aatattgtgg	caggattaat	agcaaaaaaa	a		401

&lt;210&gt; 375

&lt;211&gt; 401

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 375

gagcggagtc	cgctggctga	cccgagcgct	ggtctccgcc	gggaaccctg	gggcatggag	60
aggtctgagt	acctcggccg	cggcgcacgc	tgcctcgccg	agccaggccg	aggacgtgag	120
ggtggagggc	tcctttcccg	tgaccatgct	tccgggagac	ggtgtggggc	ctgagctgat	180
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cctgagttag	gtgcagaata	tggcatctga	ggagaagctg	gagcaggtgc	tgagttccat	300
gaaggagaac	aaagtggcca	tcattggaaa	gattcatacc	ccgatggagt	ataaggggga	360
gctagcctcc	tatgatatgc	ggctgaggcg	taagttggac	t		401

&lt;210&gt; 376

&lt;211&gt; 284

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(284)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 376

ggaacaaggt	cgtgaaaaaa	aaggtcttgg	tgagggtgccg	ccatttcatc	tgtcctcatt	60
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cacaacctct	gtgggtccga	ggagccacta	tgaggagggc	cctgggaaga	atttgccatt	180
ttcagtgga	aacaagtgg	cggtactagc	taagatgtgt	ttgtactttg	gatctgcatt	240
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&lt;210&gt; 377

&lt;211&gt; 401

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 377

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gttttgagtt	gtaaactcct	atacccttta	ttaaaatgga	cctaattaag	tgattttatgc	120
tttgtgcaat	ttcttaaate	agatctctct	aggattgaag	ggatccatag	gtatctttca	180
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ggagaatctg	cctgcctatt	tcctctccaa	atttcagaaa	ataacacaga	gtgctatttg	360
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&lt;210&gt; 378

&lt;211&gt; 401

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 378

ccagaacaca	ggtgtcgtga	aaactacccc	taaaagccaa	aatgggaaag	gaaaagactc	60
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tgatctataa	atgcggtggc	atcgacaaaa	gaaccattga	aaaatttgag	aaggaggctg	180
ctgagatggg	aaagggctcc	ttcaagtatg	cctgggtcct	ggataaactg	aaagctgagc	240
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tgactatcat	tgatgcccc	ggacacagag	actttatcaa	aaacatgatt	acagggacat	360

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401

<210> 379  
 <211> 401  
 <212> DNA  
 <213> Homo sapien

<400> 379  
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 agacatcaat caggattcag gaagacagct tttgcggaaa atgcttaaag ggaagcatca 120  
 aggattgggtg ttgatatttg aaagttaaag agtgggtatac ttttattcag tcaacacatg 180  
 acaaattgtaa aaggcactca tttgttggtc ctggaagaag cctggcagca ttccattcag 240  
 acatctgccc tttcatcgtc ccacttttta cttattgcag tcctttcagt ctgaatattt 300  
 cctcctgacg catcttctgc cgtccgaaat gactccctgc tcccagatcc tgtagccctt 360  
 attattgaca cctttcattt agaaatttag cacatgtcac a 401

<210> 380  
 <211> 401  
 <212> DNA  
 <213> Homo sapien

<400> 380  
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 tacagtattg gaaatggatc tgtctttggt aaagatcagc ctataattct tgtgctgttg 180  
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 gatgtggcca ttcttgtggg ctccatgcc aagaagggaag gcatggagag aaaagattta 360  
 ctgaaagcaa atgtgaaaat cttcaaatcc cagggtgcag c 401

<210> 381  
 <211> 401  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(401)  
 <223> n = A,T,C or G

<400> 381  
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 aaggagcgg tggcggaaga cggggatgag ctcaggacag agccagaggc caagaagagt 180  
 aagacggccg caaagaaaaa tgacaaagag gcagcaggag agggcccagc cctgtatgag 240  
 gacccccag atcagaaaac ctcaccagc ggcaaacctg ccacactcaa gatctgctct 300  
 tggaatgtgg atgggcttcg agcctggatt aagaagaaag gattagattg ggtaaaggaa 360  
 gaagccccag atatactgtg ccttcaagag accaaatggt c 401

<210> 382  
 <211> 491  
 <212> DNA  
 <213> Homo sapien

<400> 382

158

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cccgccgctg tgcattgcag cattatttca gttcaaaatg aactatatgc ctggcaccgc      180
cagcctcatc gaggacattg aaaaaaagca cttggttctg cttcgagatg gaaggacact      240
tataggcttt ttaagaagca ttgatcaatt tgcaaactta gtgctacatc agactgtgga      300
gcgatttcat gtgggcaaaa aatacgggtg tattcctcga gggatttttg tggtcagagg      360
agaaaatgtg gtcctactag gagaaataga cttggaaaag gagagtgaca caccctcca      420
gcaagtatcc attgaagaaa ttctagaaga acaaagggtg gaacagcaga ccaagctgga      480
agcagagaag t                                     491

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&lt;210&gt; 383

&lt;211&gt; 491

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 383

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gagtccatct cagcgccttg aaaatgcagt gaaaaaacct gaagataaaa aggaagtttt      60
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&lt;210&gt; 384

&lt;211&gt; 491

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 384

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&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 385

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&lt;400&gt; 389

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ctccctagct	tcaaccacat	ggaggccacg	t			511



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tle, WA 98199 (US).

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*For two-letter codes and other abbreviations, refer to the "Guid-  
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ning of each regular issue of the PCT Gazette.*

(54) Title: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF LUNG CANCER AND METHODS FOR THEIR USE

(57) Abstract: Compositions and methods for the therapy and diagnosis of cancer, such as lung cancer, are disclosed. Compositions may comprise one or more lung tumor proteins, immunogenic portions thereof, or polynucleotides that encode such portions. Alternatively, a therapeutic composition may comprise an antigen presenting cell that expresses a lung tumor protein, or a T cell that is specific for cells expressing such a protein. Such compositions may be used, for example, for the prevention and treatment of diseases such as lung cancer. Diagnostic methods based on detecting a lung tumor protein, or mRNA encoding such a protein, in a sample are also provided.

WO 00/60077 A3

# INTERNATIONAL SEARCH REPORT

International Application No

/US 00/08560

## A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12N15/12 A61K38/17 C07K14/47 C07K16/18 A61K35/14  
C12Q1/68

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12N A61K C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P,X	WO 99 38973 A (CORIXA CORP) 5 August 1999 (1999-08-05) page 1 of sequence listing, SEQ ID NO 2 ---	1,11-23, 30
A	GÜRE ET AL: "Human lung cancer antigens recognized by autologous antibodies: definition of a novel cDNA derived from the tumor suppressor gene locus on chromosome 3p21.3" CANCER RESEARCH, US, AMERICAN ASSOCIATION FOR CANCER RESEARCH, BALTIMORE, MD, vol. 58, no. 58, 1 March 1998 (1998-03-01), pages 1034-1041-41, XP002103188 ISSN: 0008-5472 --- -/-	

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

### \* Special categories of cited documents :

- \*A\* document defining the general state of the art which is not considered to be of particular relevance
- \*E\* earlier document but published on or after the international filing date
- \*L\* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- \*O\* document referring to an oral disclosure, use, exhibition or other means
- \*P\* document published prior to the international filing date but later than the priority date claimed

- \*T\* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
- \*X\* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
- \*Y\* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.
- \*Z\* document member of the same patent family

Date of the actual completion of the international search

20 July 2000

Date of mailing of the international search report

18.10.00

Name and mailing address of the ISA

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Authorized officer

ESPEN, J

# INTERNATIONAL SEARCH REPORT

International Application No

1.../US 00/08560

## C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	<p>CHEN S-L ET AL: "Isolation and characterizaton of a novel gene expressed in multiple cancers"  ONCOGENE,GB,BASINGSTOKE, HANTS,  vol. 12, no. 4,  15 February 1996 (1996-02-15), pages  741-751-751; XP002106655  ISSN: 0950-9232</p>	
A	<p>---  WO 96 02552 A (BOLLON ARTHUR P ;CYTOCLONAL  PHARMACEUTICS INC (US); TORCZYNSKI RIC)  1 February 1996 (1996-02-01)  -----</p>	

# INTERNATIONAL SEARCH REPORT

International application No.  
PCT/US 00/08560

## Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.:  
because they relate to subject matter not required to be searched by this Authority, namely:  
  
Although claims 20,21,30 are directed to a method of treatment of the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.
2. ☐ Claims Nos.:  
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

## Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Claims 1, 11-23, 30 (partially & as far as applicable)

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.



FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

1. Claims: invention 1; Claims: in part: 1,11-23,  
30; all as far as applicable

Polypeptide encoded by a polynucleotide sequence recited in SEQ ID NO 2 or polypeptide encoded by sequences that hybridize to a sequence recited in SEQ ID NO 2. Fusion protein comprising said polypeptide. Polynucleotide encoding said fusion protein. Pharmaceutical composition/vaccine comprising said polypeptide, and method for inhibiting the development of a (lung) cancer in a patient.

inventions 2-364; Claims: in part: 1-59; all as far as applicable

As invention 1, and in addition: isolated polynucleotide; method for removing tumor cells from a biological sample; method for stimulating and/or expanding T cells specific for a lung tumor protein; isolated T cell population; method for determining/monitoring a cancer in a patient; diagnostic kit; oligonucleotide.

Subject-matter of said inventions is limited to SEQ ID NOs

8,15,16,22,24,30,32-34,36,38,40,41,46-49,52,54,59,60,65-69,79,89,90,93,99-101,109-111,116-119,123-132,138-142,143,148,149,156,168,170-182,184,189,191-193,196,205,207,210-212,214,215,217-404,406,409-417,419-423,425,427-429,433-436,438-441,443,446-451,454,455,457-461,476,477,479,483,488,491,492,497,498,500,510,519,527,528,543,545,547,553,556,559,561,564,565,568,569,574-577,579,580,584,585,587,592,595,598,603,608,610,613,621-623,626,642,648,668;

wherein

invention 2 is limited to SEQ ID NO 8  
invention 3 is limited to SEQ ID NO 15, etc...  
invention 364 is limited to SEQ ID NO 668

# INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

CT/US 00/08560

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 9938973 A	05-08-1999	AU 2344399 A	16-08-1999
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WO 9602552 A	01-02-1996	US 5589579 A	31-12-1996
		AU 700915 B	14-01-1999
		AU 3359295 A	16-02-1996
		BR 9508417 A	18-11-1997
		CA 2195403 A	01-02-1996
		EP 0804451 A	05-11-1997
		JP 10503087 T	24-03-1998
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